

Query Match 100.0%; Score 982; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGNLLEDPASRDVLVYNTNMGLKIRQLLWPHISCLTTFGRETIVLEYLV 120
 DB 61 CWGELMTLATWGNLLEDPASRDVLVYNTNMGLKIRQLLWPHISCLTTFGRETIVLEYLV 120

QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 2

AAR31025
 ID AAR31025 standard; protein; 185 AA.

AC AAR31025;

XX 27-AUG-2003 (revised)

DT 19-MAY-1993 (first entry)

XX Native HBCAg protein.

DE Native HBCAg protein.

XX Native; DNA; hepatitis B; HB; core antigen; cAg; spacer; human;

KW ribosome binding site; RBS; start codon; transition; mutation;

KW frameshift; expression; host cell; antibody; blood; sample.

XX Hepatitis B virus.

OS Hepatitis B virus.

XX US5175272-A.

XX 29-DEC-1992.

XX 01-AUG-1991; 91US-00739142.

XX 01-AUG-1991; 91US-00739142.

XX (BECT) BECTON DICKINSON CO.

XX Mallonee RL;

XX WPI; 1993-026995/03.

DR N-PSDB; AAQ35322.

XX DNA sequences encoding hepatitis-B core antigen - provide increased

PT expression of HBCAg prods., for use in detection of antibodies.

XX Disclosure; Col 15-18; 21pp; English.

XX This sequence represents the native protein sequence of hepatitis B (HB)

CC core antigen (cAg). The sequences given in AAR31026-30 are altered HBCAg

CC molecules. The native DNA sequence has an 8 bp spacer between the

CC ribosome binding site (RBS) and start codon. The altered sequences may

CC contain longer spacers, transition mutations and frameshifts. Due to

CC these mutations expression was increased in host cells. The products may

CC be used to detect the presence of antibodies and thereby detect HB virus

CC infected human and blood samples. (Updated on 27-AUG-2003 to correct OS

CC field.)

XX Sequence 185 AA;

SQ

Query Match 100.0%; Score 982; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;

Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGNLLEDPASRDVLVYNTNMGLKIRQLLWPHISCLTTFGRETIVLEYLV 120
 DB 61 CWGELMTLATWGNLLEDPASRDVLVYNTNMGLKIRQLLWPHISCLTTFGRETIVLEYLV 120

QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 3

AAR30780
 ID AAR30780 standard; protein; 185 AA.

AC AAR30780;

XX 19-MAY-1993 (first entry)

DT Native HBCAg protein.

DE Native; DNA; hepatitis B; HB; core antigen; cAg; spacer; human;

KW ribosome binding site; RBS; start codon; transition; mutation;

KW frameshift; expression; host cell; antibody; blood; sample.

XX Hepatitis B virus.

OS US5175094-A.

XX 29-DEC-1992.

XX 01-AUG-1991; 91US-00739643.

XX 01-AUG-1991; 91US-00739643.

XX (BECT) BECTON DICKINSON CO.

XX Mallonee RL;

XX WPI; 1993-026939/03.

DR N-PSDB; AAQ34943.

XX Expression of hepatitis B core antigen - using modified DNA sequences to

PT increase expression of HBCAg for use in detection of antibodies.

XX Disclosure; Col 15-18; 21pp; English.

XX This sequence represents the native protein sequence of hepatitis B (HB)

CC core antigen (cAg). The sequences given in AAR30781-84 are altered HBCAg

CC molecules. The native DNA sequence has an 8 bp spacer between the

CC ribosome binding site (RBS) and start codon. The altered sequences may

CC contain longer spacers, transition mutations and frameshifts. Due to

CC these mutations expression was increased in host cells. The products may

CC be used to detect the presence of antibodies and thereby detect HB virus

CC infected human and blood samples

XX Sequence 185 AA;

SQ

Query Match 100.0%; Score 982; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATVWGNLDPASRDVAVVYNTNMGKIQRLWFIHISCLTFRGRTVLEYLV 120
 DB 61 CWGELMTLATVWGNLDPASRDVAVVYNTNMGKIQRLWFIHISCLTFRGRTVLEYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 4
 AAR55284
 ID AAR55284 standard; protein; 185 AA.
 XX AC AAR55284;
 XX DT 25-MAR-2003 (revised)
 XX DT 02-JAN-1995 (first entry)
 XX DE Deduced sequence of full length HBV core antigen in plasmid pCODM/24.
 XX KW Core antigen; recombinant replicable vaccinia virus; hepatitis;
 KW prevention; therapy; epitope; hepatitis B virus.
 XX OS Hepatitis B virus.
 XX FN W09412617-A1.
 XX PD 09-JUN-1994.
 XX PF 24-NOV-1993; 93WO-US011474.
 XX PR 25-NOV-1992; 92US-00982211.
 XX PA (ITBI-) INT BIOTECHNOLOGY LAB INC.
 XX PI Souw PTS, Okeefe RW, Lewis T, Bernstine EG;
 XX WPI; 1994-200247/24.
 XX DR N-PSDB; AAQ67964.
 XX PT Prevention and treatment of hepatitis - using recombinant replicable
 PT vaccinia viruses contg. hepatitis B virus surface and core antigen
 PT nucleotide sequences.
 XX PS Claim 11; Fig 33; 252pp; English.
 XX CC HBV core antigen (Ag) encoding sequences were subcloned and engineered so
 CC as to be transcriptionally controlled by a vaccinia or vaccinia-like
 CC promoter. A deleted version of the core gene, referred to as core delta
 CC 8, in which 8 AAs are deleted, was used. This is AAQ67963/R55283 in
 CC pT7T3/CODM. pCODM/24 is identical to pT7T3 CODM except that pCODM/24
 CC contains 24 bp which are deleted in pT7T3/CODM. The sequences of the core
 CC region in pCODM/24 are given in AAQ67964/R55284. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX SQ Sequence 185 AA;

Query Match 100.0%; Score 982; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDYKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 DB 1 MDIDYKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATVWGNLDPASRDVAVVYNTNMGKIQRLWFIHISCLTFRGRTVLEYLV 120
 DB 61 CWGELMTLATVWGNLDPASRDVAVVYNTNMGKIQRLWFIHISCLTFRGRTVLEYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 5
 AAU80940
 ID AAU80940 standard; protein; 185 AA.
 XX AC AAU80940;
 XX DT 09-APR-2002 (first entry)
 XX DE Hepatitis B virus core antigen variant (HBCAg) #45.
 XX KW Vaccine; molecular scaffold; pilus; pilin; HBCAg; antigen;
 KW hepatitis B virus capsid protein; JUN; FOS; HIV gp140;
 KW measles virus N protein; bee venom phospholipase; Th type 2 T-helper;
 KW Th2; Sinbis virus E2 protein; amyloid beta; influenza M2 antigen;
 KW human immunodeficiency virus infection; viral hepatitis; measles;
 KW chicken pox; pneumonia; tuberculosis; syphilis; malaria; allergy; cancer;
 KW chronic disease; arthritis; colitis; diabetes; multiple sclerosis.
 XX OS Hepatitis B virus.
 XX FN W0200185208-A2.
 XX PD 15-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-18000741.
 XX PR 05-MAY-2000; 2000US-0202341P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PA (SEBB/) SEBBEL F.
 XX PA (DUNA/) DUNANT N.
 XX PA (BACH/) BACHMANN M.
 XX PA (TISS/) TISSOT A.
 XX PA (LECH/) LECHENER F.
 XX PI Sebbel P, Dunant N, Bachmann M, Tissot A, Lechener F;
 XX WPI; 2002-0555561/07.
 XX DR N-PSDB; ABK23904.
 XX PT New composition, useful for vaccine production, comprises antigen or
 PT antigenic determinant and non-natural molecular scaffold comprising
 PT organizer and core particle such as bacterial pilus or pilin protein.
 XX PS Claim 34; Page 244; 287pp; English.
 XX CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold (molecular scaffold) which comprises a core particle
 CC such as a bacterial pilus or pilin protein, a recombinant form of the
 CC protein, a virus-like particle or a hepatitis B virus capsid protein
 CC (HBCAg), and an organizer; and (b) an antigen or antigenic determinant,
 CC where the molecular scaffold and antigenic determinant interact to form
 CC an ordered and repetitive antigen array. Suitable antigenic determinants
 CC include JUN, FOS, HIV gp140, measles virus N protein, bee venom
 CC phospholipase, Sinbis virus E2 protein, amyloid beta derived peptides and
 CC influenza M2 antigen. The composition (or vaccine) is useful for
 CC immunisation, by administration to a subject, where the administration
 CC produces an immune response, such as humoral, cellular or protective
 CC immune response, preferably a Th type 2 T-helper (Th2) response that is
 CC specific for the antigenic determinant. The administration induces
 CC antibodies specific for the antigenic determinant of a subtype
 CC corresponding to the Th2 subtype in the subject. The subject does not
 CC generate a Th2 subtype that is specific for pilus or pilin polypeptide or

CC antigenic determinant. The composition is useful for the production of
 CC vaccines for prevention of infectious diseases such as human
 CC immunodeficiency virus, viral hepatitis, measles, chicken pox, pneumonia,
 CC tuberculosis, syphilis, malaria, and for treating allergy, cancer, and
 CC chronic diseases induced or accelerated by a Th1 type immune response,
 CC such as arthritis, colitis, diabetes and multiple sclerosis. The
 CC composition is useful to generate defined self-specific antibodies and
 CC specific immune responses of the Th2 type and allows the creation of
 CC highly efficient vaccines against infectious diseases, and for treating
 CC allergy, cancer, and chronic diseases induced or accelerated by a Th1
 CC type immune response. The present sequence is a fusion protein
 CC incorporated into the compositions of the invention
 XX
 SQ Sequence 185 AA;

Query Match 100.0%; Score 982; DB 5; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHTALRQAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHTALRQAIL 60

QY 61 CWGELMTLATVWGNLDPASRDLVVYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
 DB 61 CWGELMTLATVWGNLDPASRDLVVYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 6
 ABG94216
 ID ABG94216 standard; protein; 185 AA.
 XX
 AC ABG94216;
 DT 10-DEC-2002 (first entry)
 XX
 DE Hepatitis B capsid (core) protein antigen (HbcAg) variant #46.
 XX
 KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KW cytotatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KW vaccine; infectious disease.
 XX
 OS Hepatitis B virus.
 XX
 PN W020256905-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB000166.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
 PI Plossek C;
 XX
 DR WPI; 2002-627351/67.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 XX diseases.

PS Claim 112; Page 365; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention
 XX

SQ Sequence 185 AA;

Query Match 100.0%; Score 982; DB 5; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHTALRQAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHTALRQAIL 60

QY 61 CWGELMTLATVWGNLDPASRDLVVYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
 DB 61 CWGELMTLATVWGNLDPASRDLVVYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 7
 ABG80528
 ID ABG80528 standard; protein; 185 AA.
 XX
 AC ABG80528;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus core capsid protein, HbcAg, isotype.
 XX
 KW Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IGH-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX
 OS Hepatitis B virus.

XX WO200256907-A2.
 XX PD 25-JUL-2002.
 XX PF 21-JAN-2002; 2002WO-IB000168.
 XX PR 19-JAN-2001; 2001US-0262379P.
 XX PR 04-MAY-2001; 2001US-0288549P.
 XX PR 05-OCT-2001; 2001US-0326998P.
 XX PR 07-NOV-2001; 2001US-0331045P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PA (NOVS) NOVAARTIS PHARMA AG.
 XX PA (MAUR/) MAURER P.
 XX PA (LECH/) LECHNER F.
 XX PA (ORTM/) ORTMANN R.
 XX PA (LUEB/) LUEBEND R.
 XX PA (STAU/) STAUFENBIEL M.
 XX PA (FREY/) FREY P.
 XX FI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 XX FI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX DR WPI; 2002-636514/68.
 XX DR N-P9DB; ABS66412.
 XX PT Molecular antigen array used in the production of vaccines for infectious diseases.
 XX PS Claim 14; Page 342-343; 418pp; English.
 XX CC The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (i) a core particle selected from: (1) a core particle of a non-natural origin; and (2) a core particle of natural origin; and (ii) an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond; (b) an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and where the second attachment site is selected from: (i) an attachment site not naturally occurring with the antigen or antigenic determinant; and (ii) an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site; and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. Also included is a process for producing a non-naturally occurring ordered and repetitive antigen array. The composition is used in immunisation and as a vaccine for diseases such as influenza, graft versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease, systemic lupus erythematosus, inflammatory immune diseases, myasthenia gravis, immunoproliferative disease lymphadenopathy, angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy, rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis and infectious diseases. The present sequence is an antigen for use in the array of the invention. The antigen is modified to possess a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N- or C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein)

XX Query Match 100.0%; Score 982; DB 5; Length 185;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 XX Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Sequence 185 AA;
 QY 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
 Db 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWVGNNLEDPASRDLVVNYVNTNMGLKIRQLLWFHISCLTFCRETVEVLV 120
 Db 61 CWGELMTLATWVGNNLEDPASRDLVVNYVNTNMGLKIRQLLWFHISCLTFCRETVEVLV 120
 QY 121 SFGWIRTTPAYRPPNAPILSTLPETTVARRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 Db 121 SFGWIRTTPAYRPPNAPILSTLPETTVARRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 QY 181 RESQC 185
 Db 181 RESQC 185

RESULT 8
 AAM50944
 ID AAM50944 standard; protein; 185 AA.
 XX AC AAM50944;
 XX DT 07-AUG-2003 (revised)
 XX DT 15-MAY-2002 (first entry)
 XX DE Hepatitis B virus core antigen.
 XX KW IgE; immunoglobulin E; human; allergy; asthma; eczema; urticaria;
 KW anaphylactic shock; allergic rhinitis; conjunctivitis; antianaphylactic;
 KW immunosuppressive; antiallergic; antiasthmatic; antiinflammatory;
 KW dermatological; vasotropic; ophthalmological; vaccine; therapy;
 KW core antigen; HBcAg; carrier protein.
 XX OS Hepatitis B virus.
 XX PN WO200209751-A2.
 XX PD 07-FEB-2002.
 XX PF 27-JUL-2001; 2001WO-IB001353.
 XX PR 28-JUL-2000; 2000US-0221841P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PA (BACH/) BACHMANN M F.
 XX PA (RENN/) RENNER W A.
 XX PI Bachmann MF, Renner WA;
 XX WPI; 2002-227076/28.
 XX CC Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CH1 and/or CH4 domains of IgE molecule coupled to a carrier.
 XX Disclosure; Page 59-60; 71pp; English.
 XX The present sequence is that of the hepatitis B virus core antigen (HBcAg) generated by removal of the 29 N-terminal amino acids from the 214-amino acid HBcAg precursor protein. HBcAg can be used as a carrier in compositions of the invention that induce self-specific anti-IgE antibodies. Claimed compositions contain carriers foreign to the immunised mammal, such as HBcAg, coupled to polypeptides containing fragments of an IgE molecule (see AAM50940), especially fragments including the constant CH1 and/or CH4 domain. A fusion protein comprising the carrier protein and IgE-derived polypeptide, or a polynucleotide encoding the fusion protein, may be administered to the mammal. The resulting anti-IgE antibodies reduce or eliminate the pool of free IgE in the mammal's serum. The compositions and polynucleotides are used to inhibit or treat IgE-mediated disorders such as anaphylactic shock, allergic rhinitis or conjunctivitis, an allergic reaction to an allergen such as fur, dust or food, an asthmatic reaction, eczema or urticaria (all claimed). Viral-based carriers induce prompt and efficient immune responses in the absence of any adjuvants both with and without T-cell help. (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 185 AA;
 Query Match 100.0%; Score 982; DB 5; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEFGATVVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 QY 61 CWGELMTLATWVGNLDPASRLVNVYNTNMGLKIRQLLWFIHISCLTFGRVTVLEYLV 120
 DB 61 CWGELMTLATWVGNLDPASRLVNVYNTNMGLKIRQLLWFIHISCLTFGRVTVLEYLV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 9
 ABG70773
 ID ABG70773 standard; protein; 185 AA.
 AC ABG70773;
 XX
 DT 06-AUG-2002 (revised)
 DT 09-DEC-2002 (first entry)
 XX
 DE Hepatitis B virus (HBV) core antigen (HBe) protein.
 XX
 KW HBV; core antigen; HBe; stress protein; heat shock protein; Hsp65;
 KW immune response; non-cytopathic DNA virus; vaccine; morbidity; mortality;
 KW infection; gene therapy; hepatitis; cirrhosis; hepatocellular carcinoma;
 KW virucide; immunostimulant; hepatotropic; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 FH Key Location/Qualifiers
 FT Region 87..95
 FT /note= "Cytotoxic T lymphocyte epitope"
 FT Region 93..100
 FT /note= "Murine cytotoxic T lymphocyte epitope"
 XX
 PN W0200262959-A2.
 XX
 XX 15-AUG-2002.
 XX
 XX 05-FEB-2002; 2002WO-US003460.
 XX
 XX 05-FEB-2001; 2001US-0266733P.
 XX
 XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX
 XX Mizzen L, Liu H, Siegel M;
 XX WPI; 2002-706903/76.
 XX N-PSDB; ABS54444.
 XX
 XX Novel isolated fusion protein useful for treating hepatitis B virus
 XX infection in a subject, comprises a stress protein or its portion, and a
 XX hepatitis B virus core antigen.
 XX
 XX Example 1; Fig 2; 58pp; English.
 XX
 XX The invention discloses an isolated fusion protein, and the
 XX polynucleotide encoding it, that comprises a stress protein (e.g.
 XX Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
 XX hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,

CC when administered to an individual, induces or enhances an immune
 CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus
 CC against which a vaccine has been developed. However, due to the morbidity
 CC and mortality arising from chronic HBV infection occurring over a period
 CC of decades, the impact of vaccinations will not be apparent for some time
 CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
 CC therapy and as a pharmaceutical composition for inducing or enhancing an
 CC immune response against an HBV core antigen in a subject for treating an
 CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
 CC The sequence presented is the hepatitis B virus core antigen protein.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 185 AA;
 Query Match 100.0%; Score 982; DB 5; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 1 MDIDPYKEFGATVVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 QY 61 CWGELMTLATWVGNLDPASRLVNVYNTNMGLKIRQLLWFIHISCLTFGRVTVLEYLV 120
 DB 61 CWGELMTLATWVGNLDPASRLVNVYNTNMGLKIRQLLWFIHISCLTFGRVTVLEYLV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 10
 ABR56506
 ID ABR56506 standard; protein; 185 AA.
 XX
 AC ABR56506;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Hepatitis B core antigen precursor variant protein SEQ ID NO:77.
 XX
 KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antithyroid; antidiabetic; neuroprotective; nontropic; osteopathic;
 KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 OS Hepatitis B virus.
 OS Synthetic.
 XX
 XX W02003024480-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 16-SEP-2002; 2002WO-IB004252.
 XX
 XX 14-SEP-2001; 2001US-0318967P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann MF, Storni T, Lechner F;
 XX WPI; 2003-363095/34.
 XX
 XX A composition, useful for enhancing an immune response against an antigen
 PT

PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.

PS Disclosure; Page 235-236; 243pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention

XX Sequence 185 AA;

Query Match 100.0%; Score 982; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRAIL 60

Qy 61 CWGELMTLATWVGNLDPASRLDVVNTNMGKIRQLLWPHISCLTFGRETVLYLV 120
 Db 61 CWGELMTLATWVGNLDPASRLDVVNTNMGKIRQLLWPHISCLTFGRETVLYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180

Qy 181 RESQC 185
 Db 181 RESQC 185

RESULT 11

ABU09684

ID ABU09684 standard; protein; 185 AA.

XX AC ABU09684;

XX AC ABU09684;

DT 03-JUL-2003 (first entry)

DE Modified hepatitis B capsid (core) protein HBcAg.

XX Hepatitis B capsid protein; HBcAg; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW rein-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.

XX Hepatitis B virus.

OS Synthetic.

XX WO2003031466-A2.

XX 17-APR-2003.

XX 07-OCT-2002; 2002WO-EP011219.

XX 05-OCT-2001; 2001US-0326998P.

XX 07-NOV-2001; 2001US-0331045P.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-IB000166.

XX 19-JUL-2002; 2002US-0396637P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M;

XX WPI; 2003-430264/40.

XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.

PS Claim 6; Page 91; 97pp; English.

XX The invention describes an angiotensin peptide moiety carrier conjugate
 CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC modified hepatitis B virus capsid protein HBcAg used in the preparation
 CC of the vaccine conjugates of the invention

XX Sequence 185 AA;

Query Match 100.0%; Score 982; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRAIL 60

Qy 61 CWGELMTLATWVGNLDPASRLDVVNTNMGKIRQLLWPHISCLTFGRETVLYLV 120

Db 61 CWGELMTLATWVGNLDPASRLDVVNTNMGKIRQLLWPHISCLTFGRETVLYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180

Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180

Qy 181 RESQC 185

Db 181 RESQC 185

RESULT 12

ABR44609

ID ABR44609 standard; protein; 185 AA.

XX AC ABR44609;

XX AC ABR44609;

DT 25-JUL-2003 (first entry)

XX Hepatitis B core antigen precursor variant protein SEQ ID NO:77.

DE Hepatitis B core antigen precursor variant protein SEQ ID NO:77.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;

KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
 OS Hepatitis B virus.
 OS Synthetic.
 XX WO2003024481-A2.
 XX 27-MAR-2003.
 XX 16-SEP-2002; 2002WO-1B004132.
 XX 14-SEP-2001; 2001US-0318994P.
 XX 22-APR-2002; 2002US-0374145P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER) MAURER P.
 PA (TISSOT) TISSOT A.
 PA (SCHWAB) SCHWARZ K.
 PA (MEIJER) MEIJERINK E.
 PA (LIPO) LIPOMSKY G.
 PA (PUMP) PUMPKENS P.
 PA (CIELENS) CIELENS I.
 PA (REINHOLD) REINHOLD R.
 XX Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
 XX WPI; 2003-354564/33.
 XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX Disclosure; Page 315; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
 CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention

XX Sequence 185 AA;

Query Match 100.0%; Score 982; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKFGATVLLSFLSPDPPSVRDLLDTASALYREALSPHCSPHHTALQAIL 60
 DB 1 MDIDPYKFGATVLLSFLSPDPPSVRDLLDTASALYREALSPHCSPHHTALQAIL 60

QY 61 CWGELMTLATWGNLEDPASRDLVVYVNTNMGLKIQQLWFWHISCLTFORETVLEVLV 120
 DB 61 CWGELMTLATWGNLEDPASRDLVVYVNTNMGLKIQQLWFWHISCLTFORETVLEVLV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 13

ADD24135
 ID ADD24135 standard; protein; 185 AA.

XX AC ADD24135;

XX 15-JAN-2004 (first entry)

DT Hepatitis B virus core antigen (HBcAg) precursor wild-type protein #1.
 DE vaccine composition; virus-like particle; core particle;
 DE first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; HBcAg.

XX Hepatitis B virus.

XX WO2003059386-A2.

XX 24-JUL-2003.

XX 17-JAN-2003; 2003WO-EP000460.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-1B000166.

XX 08-JUL-2002; 2002US-0393725P.

XX 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;

XX WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phase) and at least one prion protein or peptide bound to the virus-like
 PT particle.

XX Disclosure; SEQ ID NO 28; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is the amino acid sequence of a mutant
 CC hepatitis B virus core antigen (HBcAg) which may be used during the
 CC creation of the vaccine composition of the invention.

XX Sequence 185 AA;

Query Match 100.0%; Score 982; DB 7; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;

Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHHCSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHHCSPHHTALRQAIL 60
 QY 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
 Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 QY 181 RESQC 185
 Db 181 RESQC 185

RESULT 14
 ADD24184
 ID ADD24184 standard; protein; 185 AA.
 AC ADD24184;
 DT 15-JAN-2004 (first entry)
 DE Hepatitis B virus core antigen (HBcAg) precursor wild-type protein #2.
 KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; HBcAg.
 OS Hepatitis B virus.
 XX
 XX
 PN WO2003059386-A2.
 XX
 PD 24-JUL-2003.
 XX
 XX 17-JAN-2003; 2003WO-EP000460.
 XX
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 XX
 DR WPI; 2003-598483/56.
 XX
 XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.
 XX
 XX Example 4; SEQ ID NO 77; 246pp; English.
 PS
 XX
 XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is the amino acid sequence of a mutant
 CC hepatitis B virus core antigen (HBcAg) which may be used during the
 CC creation of the vaccine composition of the invention.

XX SQ Sequence 185 AA;
 Query Match 100.0%; Score 982; DB 7; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHHCSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHHCSPHHTALRQAIL 60
 QY 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
 Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
 QY 181 RESQC 185
 Db 181 RESQC 185

RESULT 15
 ABR56438
 ID ABR56438 standard; protein; 197 AA.
 XX AC ABR56438;
 XX
 XX 28-JUL-2003 (first entry)
 XX
 DE LCMV p33 and Hepatitis B core protein fusion protein.
 XX
 KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytostatic; viricide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antihydramic; antidiabetic; neuroprotective; nontropic; osteopathic;
 KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 XX Lymphocytic choriomeningitis virus.
 OS Hepatitis B virus.
 XX
 XX WO2003024480-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 16-SEP-2002; 2002WO-IB004252.
 XX
 XX 14-SEP-2001; 2001US-0318967P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann MP, Storni T, Lechner F;
 XX
 XX WPI; 2003-363095/34.
 XX
 XX N-PSDB; ACC69850.
 XX
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunising or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX
 XX Example 1; Fig 1; 243pp; English.
 PS
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also

described: (1) enhancing an immune response against an antigen or a VLP in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral protection in an animal comprising introducing (C) into the animal. (C) has cytostatic, virucide, antibacterial, antiparasitic, fungicide, antiallergic, immunosuppressive, antiaddictive, antiinflammatory, antirheumatic and antiarthritic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or treating tumours and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509 represent sequences used in the exemplification of the present invention

XX Sequence 197 AA;
SQ

Query Match 100.0%; Score 982; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALQAIL 60

Qy 61 CWGELMTLATWGNLSDPASRDVNVNTNMGKIRQLLWPHISCLTFGRETVLEYLV 120
Db 61 CWGELMTLATWGNLSDPASRDVNVNTNMGKIRQLLWPHISCLTFGRETVLEYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180

Qy 181 RESQC 185
Db 181 RESQC 185

Search completed: July 20, 2004, 09:19:00
Job time : 55 secs

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OM protein - protein search, using sw model

Run on: July 20, 2004, 09:20:20 ; Search time: 45 Seconds
(without alignments)
1284.972 Million cell updates/sec

Title: US-10-068-059-2
Perfect score: 982
Sequence: 1 MDIDPYKEGATVELLSFLP.....RRRSQSPRRRSQSRQC 185

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1285356 seqs, 312560742 residues

Total number of hits satisfying chosen parameters: 1285356

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	982	100.0	185	9	US-09-916-230-5
2	982	100.0	185	10	US-09-848-616-134
3	982	100.0	185	12	US-10-289-456-28
4	982	100.0	185	12	US-10-289-456-77
5	982	100.0	185	12	US-10-622-064-1
6	982	100.0	185	13	US-10-068-059-2
7	982	100.0	185	14	US-10-243-739-77
8	982	100.0	185	14	US-10-048-065-77
9	982	100.0	185	14	US-10-289-454-28
10	982	100.0	185	14	US-10-289-454-77
11	982	100.0	185	14	US-10-050-902-134
12	982	100.0	185	14	US-10-050-898-134
13	982	100.0	185	15	US-10-346-190-28
14	982	100.0	185	15	US-10-346-190-77
15	982	100.0	185	15	US-10-465-811-19

16	982	100.0	185	15	US-10-465-811-68	Sequence 68, Appl
17	982	100.0	185	16	US-10-622-124-22	Sequence 22, Appl
18	982	100.0	185	16	US-10-622-124-25	Sequence 25, Appl
19	982	100.0	185	15	US-10-465-811-71	Sequence 71, Appl
20	982	100.0	236	15	US-10-365-620-37	Sequence 37, Appl
21	982	100.0	460	15	US-10-365-620-35	Sequence 35, Appl
22	979	99.7	185	10	US-09-931-325A-171	Sequence 171, App
23	979	99.7	185	10	US-09-930-915A-248	Sequence 248, App
24	979	99.7	185	12	US-10-274-616-2	Sequence 2, Appl
25	979	99.7	185	14	US-10-080-299-2	Sequence 2, Appl
26	979	99.7	185	14	US-10-082-014-2	Sequence 2, Appl
27	979	99.7	185	14	US-10-372-076-2	Sequence 12, Appl
28	978	99.6	724	13	US-10-068-059-12	Sequence 6, Appl
29	978	99.6	746	13	US-10-068-059-6	Sequence 6, Appl
30	971	98.9	185	10	US-09-931-325A-172	Sequence 172, App
31	971	98.9	185	10	US-09-930-915A-249	Sequence 249, App
32	971	98.9	185	12	US-10-274-616-3	Sequence 3, Appl
33	971	98.9	185	14	US-10-080-299-3	Sequence 3, Appl
34	971	98.9	185	14	US-10-082-014-3	Sequence 3, Appl
35	971	98.9	185	14	US-10-372-076-3	Sequence 3, Appl
36	966.5	98.4	184	14	US-10-243-739-28	Sequence 28, Appl
37	966.5	98.4	184	14	US-10-244-065-28	Sequence 28, Appl
38	962	98.0	185	15	US-10-465-811-97	Sequence 97, Appl
39	957	97.5	183	10	US-09-848-616-131	Sequence 131, App
40	957	97.5	183	12	US-10-289-456-71	Sequence 71, Appl
41	957	97.5	183	14	US-10-243-739-71	Sequence 71, Appl
42	957	97.5	183	14	US-10-244-065-71	Sequence 71, Appl
43	957	97.5	183	14	US-10-289-454-71	Sequence 71, Appl
44	957	97.5	183	14	US-10-050-902-131	Sequence 131, App
45	957	97.5	183	14	US-10-050-898-131	Sequence 131, App

ALIGNMENTS

RESULT 1

US-09-916-230-5
; Sequence 5, Application US/09916230
; Patent No. US20020146422A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin P.
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Compositions for Inducing Self-Specific Anti-Ige
; TITLE OF INVENTION: Antibodies and Uses Thereof
; FILE REFERENCE: 1700.0140001
; CURRENT APPLICATION NUMBER: US/09/916,230
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,841
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-916-230-5

Query Match	100.0%;	Score	982;	DB	9;	Length	185;
Best Local Similarity	100.0%;	Pred. No.	7.6e-91;				
Matches	185;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MDIDPYKEGATVELLSFLPDPFPVRLDLDTSALYREALSPHCHSPHHTALRAIL	60				
Db	1	MDIDPYKEGATVELLSFLPDPFPVRLDLDTSALYREALSPHCHSPHHTALRAIL	60				
Qy	61	CWGLMTLATVGNLDPASRDVAVNYVNTNMGKIRQLWPHISCLTFCGRTVLEYLV	120				
Db	61	CWGLMTLATVGNLDPASRDVAVNYVNTNMGKIRQLWPHISCLTFCGRTVLEYLV	120				
Qy	121	SFGWIRTPPAYRPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQS	180				
Db	121	SFGWIRTPPAYRPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQS	180				

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QY 181 RESQC 185
DB 181 RESQC 185

RESULT 2
US-09-848-616-134
; Sequence 134, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 134
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-848-616-134

Query Match 100.0%; Score 982; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVELLSPLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPKFGATVELLSPLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRETVEYL 120
DB 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRRSQSPRRRSQS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRRSQSPRRRSQS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 3
US-10-289-456-28
; Sequence 28, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-289-456-28

Query Match 100.0%; Score 982; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVELLSPLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPKFGATVELLSPLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRETVEYL 120
DB 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRRSQSPRRRSQS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRRSQSPRRRSQS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 4
US-10-289-456-77
; Sequence 77, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 77
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-289-456-77

Query Match 100.0%; Score 982; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVELLSPLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPKFGATVELLSPLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRETVEYL 120
DB 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRRSQSPRRRSQS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRRSQSPRRRSQS 180
QY 181 RESQC 185
DB 181 RESQC 185
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RESULT 5
US-10-622-064-1
; Sequence 1, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-622-064-1

Query Match      100.0%; Score 982; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120
Db      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120

Qy      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy      181 RESQC 185
Db      181 RESQC 185

RESULT 6
US-10-068-059-2
; Sequence 2, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-068-059-2

Query Match      100.0%; Score 982; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120
Db      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120

Qy      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy      181 RESQC 185
Db      181 RESQC 185

RESULT 7
US-10-243-739-77
; Sequence 77, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement o
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-243-739-77

Query Match      100.0%; Score 982; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120
Db      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120

Qy      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy      181 RESQC 185
Db      181 RESQC 185

RESULT 8
US-10-244-065-77
; Sequence 77, Application US/10244065
; Publication No. US2003009968A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhota, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Partic
; TITLE OF INVENTION: Method of Preparation and Use
```

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Db      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120
Qy      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy      181 RESQC 185
Db      181 RESQC 185

RESULT 7
US-10-243-739-77
; Sequence 77, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement o
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-243-739-77

Query Match      100.0%; Score 982; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db      1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120
Db      61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVLEVLYV 120

Qy      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db      121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy      181 RESQC 185
Db      181 RESQC 185

RESULT 8
US-10-244-065-77
; Sequence 77, Application US/10244065
; Publication No. US2003009968A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhota, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Partic
; TITLE OF INVENTION: Method of Preparation and Use
```

FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patent in version 3.1
SEQ ID NO 77
LENGTH: 185
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-244-065-77

Query Match 100.0%; Score 982; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
DB 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSOS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSOS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 9
US-10-289-454-28
Sequence 28, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patent in version 3.2
SEQ ID NO 28
LENGTH: 185
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-289-454-28

Query Match 100.0%; Score 982; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120

DB 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSOS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSOS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 10
US-10-289-454-77
Sequence 77, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patent in version 3.2
SEQ ID NO 77
LENGTH: 185
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-289-454-77

Query Match 100.0%; Score 982; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
DB 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSOS 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSOS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 11
US-10-050-902-134
Sequence 134, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Sebbel, Peter
APPLICANT: Fiossek, Christine

```
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-050-902-134

Query Match      100.0%; Score 982; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDIDPYKEFGATVLLSPDPPSVRDLLDTASALYREALSPHCHSPHHTALRQAIL 60
DB      1 MDIDPYKEFGATVLLSPDPPSVRDLLDTASALYREALSPHCHSPHHTALRQAIL 60
QY      61 CWGELMTLATWVGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
DB      61 CWGELMTLATWVGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
QY      121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB      121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
QY      181 RESQC 185
DB      181 RESQC 185

RESULT 12
US-10-346-190-28
; Sequence 28, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-346-190-28

Query Match      100.0%; Score 982; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDIDPYKEFGATVLLSPDPPSVRDLLDTASALYREALSPHCHSPHHTALRQAIL 60
DB      1 MDIDPYKEFGATVLLSPDPPSVRDLLDTASALYREALSPHCHSPHHTALRQAIL 60
QY      61 CWGELMTLATWVGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
DB      61 CWGELMTLATWVGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
QY      121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB      121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
QY      181 RESQC 185
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Db 181 RESQC 185

RESULT 14

US-10-346-190-77
; Sequence 77, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-346-190-77

Query Match 100.0%; Score 982; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Qy 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 15

US-10-465-811-19
; Sequence 19, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; TITLE OF INVENTION: METHOD OF PREPARATION AND USE
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19

; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-465-811-19
Query Match 100.0%; Score 982; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Qy 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWPHISCLTFGRETVEYL 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

Search completed: July 20, 2004, 09:25:48
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2004, 09:15:39 ; Search time 39 Seconds
(without alignments)
1496.689 Million cell updates/sec

Title: US-10-068-059-2

Perfect score: 982
Sequence: 1 MDIDPYKEFGATVLLSFLP.....RRRSQSFRRRSQRSSQ 185

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organalle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	982	100.0	185	12 Q67855	Q67855 hepatitis b
2	982	100.0	214	12 Q910H6	Q910H6 hepatitis b
3	982	100.0	214	12 Q3WRK6	Q3WRK6 hepatitis b
4	982	100.0	214	12 Q81106	Q81106 hepatitis b
5	982	100.0	214	12 Q15194	Q15194 hepatitis b
6	980	99.8	214	12 Q91T09	Q91T09 hepatitis b
7	979	99.7	214	12 Q910F2	Q910F2 hepatitis b
8	979	99.7	214	12 Q91C44	Q91C44 hepatitis b
9	977	99.5	185	12 Q8VBG0	Q8VBG0 hepatitis b
10	977	99.5	214	12 Q67894	Q67894 hepatitis b
11	976	99.4	185	12 Q91E11	Q91E11 hepatitis b
12	976	99.4	185	12 Q8TXG8	Q8TXG8 hepatitis b
13	976	99.4	214	12 Q91E12	Q91E12 hepatitis b
14	975	99.3	185	12 Q8VBG6	Q8VBG6 hepatitis b
15	975	99.3	185	12 Q8BCB5	Q8BCB5 hepatitis b
16	975	99.3	214	12 Q91C37	Q91C37 hepatitis b

17	975	99.3	214	12 Q8BCB6	Q8BCB6 hepatitis b
18	974	99.2	185	12 Q8VBG8	Q8VBG8 hepatitis b
19	973	99.1	185	12 Q91E17	Q91E17 hepatitis b
20	973	99.1	185	12 Q8VBG5	Q8VBG5 hepatitis b
21	973	99.1	185	12 Q8AZ51	Q8AZ51 hepatitis b
22	973	99.1	214	12 Q91T08	Q91T08 hepatitis b
23	973	99.1	214	12 Q91T07	Q91T07 hepatitis b
24	973	99.1	214	12 Q91E18	Q91E18 hepatitis b
25	973	99.1	214	12 Q81105	Q81105 hepatitis b
26	973	99.1	214	12 Q8AZ33	Q8AZ33 hepatitis b
27	972	99.0	185	12 Q67868	Q67868 hepatitis b
28	972	99.0	185	12 Q8VBG1	Q8VBG1 hepatitis b
29	971	98.9	185	12 Q8B4N3	Q8B4N3 hepatitis b
30	971	98.9	214	12 Q8B4N4	Q8B4N4 hepatitis b
31	970	98.8	185	12 Q91EH4	Q91EH4 hepatitis b
32	970	98.8	214	12 Q91EH5	Q91EH5 hepatitis b
33	970	98.8	214	12 Q91532	Q91532 hepatitis b
34	969	98.7	185	12 Q8JNW2	Q8JNW2 hepatitis b
35	969	98.7	214	12 Q8JNW3	Q8JNW3 hepatitis b
36	968	98.6	185	12 Q8VBH4	Q8VBH4 hepatitis b
37	965	98.3	214	12 Q91T10	Q91T10 hepatitis b
38	962	98.0	185	12 Q8VBG3	Q8VBG3 hepatitis b
39	962	98.0	214	12 Q9WP82	Q9WP82 hepatitis b
40	961	97.9	214	12 Q917H9	Q917H9 hepatitis b
41	960	97.8	185	12 Q8QXR0	Q8QXR0 hepatitis b
42	960	97.8	185	12 Q8VBG4	Q8VBG4 hepatitis b
43	960	97.8	185	12 Q8VBG2	Q8VBG2 hepatitis b
44	960	97.8	214	12 Q8QXR1	Q8QXR1 hepatitis b
45	957	97.5	183	12 Q9QBF7	Q9QBF7 hepatitis b

ALIGNMENTS

RESULT 1

Q67855 ID Q67855 PRELIMINARY; PRT; 185 AA.
AC Q67855;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE HBCAG protein (Core protein).
GN C OR CORE.
OS Hepatitis B virus.
OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_taxid=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A317;
RA Schories M., Schlauer H., Rasenack J.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Heermann K.H., Gerlich W.H., Chudy M., Schaefer S., Reiner T.;
RT "Quantitative Determination of Hepatitis B Virus DNA in two International Reference Plasmas."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=I68, U9, 8.21, 7.32, and I60;
RA Jazayeri M., Sran N., Gish R., Basuni A.A., Cooksley G., Locarnini S., Carman W.P.;
RT "HBV core sequence: definition of genotype-specific variability and correlation with geographic origin."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Roch G.J., Osioy C.K.;
RT "Sequencing of full-length HBV genome insert present in pECO63."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Vaishali C., Acharya S.K., Panda S.K.;

RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
 RT sequence of HBV from nine patients with seronegative viral
 RL hepatitis";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: 72478; CAA96554.1; -;
 DR EMBL: AJ012207; CAA09961.1; -;
 DR EMBL: AF324148; AAL31861.1; -;
 DR EMBL: AF324125; AAL31838.1; -;
 DR EMBL: AF324128; AAL31841.1; -;
 DR EMBL: AF324136; AAL31849.1; -;
 DR EMBL: AF324147; AAL31860.1; -;
 DR EMBL: AY128092; AAM96931.1; -;
 DR EMBL: AY161138; AAO12547.1; -;
 DR EMBL: AY161139; AAO12554.1; -;
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 185 AA; 21395 MW; D3073D6391FB64A8 CRC64;

Query Match 100.0%; Score 982; DB 12; Length 185;
 Best Local Similarity 100.0%; Pred. No. 2.6e-93;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60

QY 61 CWGELMTLATWGNLDDPASRDVLVYNTNMGKIRQLLWPHISCLTFGRTVLEYLV 120
 DB 61 CWGELMTLATWGNLDDPASRDVLVYNTNMGKIRQLLWPHISCLTFGRTVLEYLV 120

QY 121 SPGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
 DB 121 SPGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180

QY 181 RESQC 185
 DB 181 RESQC 185

RESULT 2

Q910H6 PRELIMINARY; PRT; 214 AA.
 ID AC Q910H6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Precore/core protein.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC STRAIN=Various strains;
 RA Dumps U., Mandy M., Karayiannis P.;
 RT "Prevalence of HBV core promoter/precure/core mutations in Gambian
 RT chronic carriers";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF350098; AAK57215.1; -;
 DR EMBL: AF350080; AAK57197.1; -;
 DR EMBL: AF350082; AAK57199.1; -;
 DR EMBL: AF350084; AAK57201.1; -;
 DR EMBL: AF350085; AAK57202.1; -;
 DR EMBL: AF350088; AAK57205.1; -;
 DR EMBL: AF350089; AAK57206.1; -;
 DR EMBL: AF350090; AAK57207.1; -;
 DR EMBL: AF350091; AAK57208.1; -;
 DR EMBL: AF350092; AAK57209.1; -;
 DR EMBL: AF350093; AAK57210.1; -;
 DR EMBL: AF350094; AAK57211.1; -;
 DR EMBL: AF350095; AAK57212.1; -;
 DR EMBL: AF350096; AAK57213.1; -;
 DR EMBL: AF350097; AAK57214.1; -;
 PIR: C94409; NKVLA3.

DR PIR: S33686; S33686.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 214 AA; 24657 MW; BF80D7A1E06B5AEB CRC64;

Query Match 100.0%; Score 982; DB 12; Length 214;
 Best Local Similarity 100.0%; Pred. No. 3.1e-93;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 DB 30 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89

QY 61 CWGELMTLATWGNLDDPASRDVLVYNTNMGKIRQLLWPHISCLTFGRTVLEYLV 120
 DB 90 CWGELMTLATWGNLDDPASRDVLVYNTNMGKIRQLLWPHISCLTFGRTVLEYLV 149

QY 121 SPGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
 DB 150 SPGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 209

QY 181 RESQC 185
 DB 210 RESQC 214

RESULT 3

Q9WRK6 PRELIMINARY; PRT; 214 AA.
 ID AC Q9WRK6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Precore+core.
 GN PRECORB+CORE.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC STRAIN=G3.27270;
 RX MEDLINE=99278305; PubMed=10347133;
 RA Stuyver L., De Gendt S., Cadanel J.F., Van Geyt C., Van Reybroeck G.,
 Dorent R., Gandjbachkh I., Rosenheim M., Charlotte P., Opolon P.,
 Huraux J.M., Lunel F.;
 RT "Three cases of severe subfulminant hepatitis in heart-transplanted
 RT patients after nosocomial transmission of a mutant hepatitis B
 RT virus";
 RL Hepatology 29:1876-1883(1999).
 RN [2];
 RP SEQUENCE FROM N.A.
 RC STRAIN=G3.27270;
 RA Stuyver L.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF090840; AAD40210.1; -;
 DR PIR: C94409; NKVLA3.
 DR PIR: S33686; S33686.
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 214 AA; 24701 MW; B5D750322E418E02 CRC64;

Query Match 100.0%; Score 982; DB 12; Length 214;
 Best Local Similarity 100.0%; Pred. No. 3.1e-93;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
 DB 30 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89

QY 61 CWGELMTLATWGNLDDPASRDVLVYNTNMGKIRQLLWPHISCLTFGRTVLEYLV 120
 DB 90 CWGELMTLATWGNLDDPASRDVLVYNTNMGKIRQLLWPHISCLTFGRTVLEYLV 149

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Qy 121 SFGWIRTPPAYRPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQS 180
Db 150 SFGWIRTPPAYRPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQS 209

Qy 181 RESQC 185
Db 210 RESQC 214

RESULT 4
Q81106 PRELIMINARY; PRT; 214 AA.
AC Q81106;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF1 (Pre-C/C).
GN PRE-C/C OR PRECORE+CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91251207; PubMed=2041082;
RA Tran A., Kremendorf D., Capel F., Housset C., Dauguet C., Petit M.A.,
RA Brechot C.;
RT "Emergence of and takeover by hepatitis B virus (HBV) with
RT rearrangements in the pre-S/S and pre-C/C genes during chronic HBV
RT infection.";
RL J. Virol. 65:3566-3574 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=G5.27295;
RA Stuyver L., De Gendt S., Cadranet J.F., Van Geyt C., Van Reybroeck G.,
RA Dorent R., Gandjbachkh I., Rosenheim M., Opolon P., Huraux J.M.,
RA and Lunel F.;
RT "Three cases of severe sub-fulminant hepatitis in heart transplanted
RT patients after nosocomial transmission of a mutant hepatitis B
RT virus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=G4.27241, and G2.27245;
RA Stuyver L., De Gendt S., Cadranet J.F., Van Geyt C., Van Reybroeck G.,
RA Dorent R., Gandjbachkh I., Rosenheim M., Opolon P., Huraux J.M.,
RA and Lunel F.;
RT "Three cases of severe sub-fulminant hepatitis in heart transplanted
RT patients after nosocomial transmission of a mutant hepatitis B
RT virus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=G4.27241, and G2.27245;
RA Stuyver L., De Gendt S., Cadranet J.F., Van Geyt C., Van Reybroeck G.,
RA Dorent R., Gandjbachkh I., Rosenheim M., Opolon P., Huraux J.M.,
RA and Lunel F.;
RT "Three cases of severe sub-fulminant hepatitis in heart transplanted
RT patients after nosocomial transmission of a mutant hepatitis B
RT virus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=80;
RX MEDLINE=21479634; PubMed=11596083;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Molecular analysis of hepatitis B virus genomes isolated from black
RT African patients with fulminant hepatitis B.";
RL J. Med. Virol. 65:485-492 (2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=80;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RX MEDLINE=21361467; PubMed=11468728;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults
RT positive for hepatitis B surface antibody alone: possible association
RT with recombination between genotypes A and D.";
RL J. Med. Virol. 64:441-454 (2001).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA Owiredu W.K.B.A., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA Owiredu W.K.B.A., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV-Mal14;
RA Sugauchi F., Orito E., Kato H., Suzuki S., Hasegawa I., Sakurai M.,
RA Yoshihara N., Ueda R., Mizokami M.;
RT "Hepatitis B virus isolates in Malawi: genotypes, HBsAg subtypes and
RT phylogenetic characterization.";

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PREC (HBsAg) (HBsAg/HBcAg) (PreC/core protein) (Precore).
GN PRECORE+CORE OR PRECORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Meisel H., Jantschak J., Tars K., Prosch S., Pushko P., Pumpens P.;
RT "Nucleotide sequence of HBV adw variant.";
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A317;
RA Schories M., Schlager H., Rasenack J.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88335570; PubMed=3419915;
RA Cheng S., Vogel R., Ye R., Blume M., Lee S., Hung P.;
RT "The core gene of hepatitis B virus; subtype adw2.";
RL Nucleic Acids Res. 16:8188-8188 (1988).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=G4.27241, and G2.27245;
RA Stuyver L., De Gendt S., Cadranet J.F., Van Geyt C., Van Reybroeck G.,
RA Dorent R., Gandjbachkh I., Rosenheim M., Opolon P., Huraux J.M.,
RA and Lunel F.;
RT "Three cases of severe sub-fulminant hepatitis in heart transplanted
RT patients after nosocomial transmission of a mutant hepatitis B
RT virus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=80;
RX MEDLINE=21479634; PubMed=11596083;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Molecular analysis of hepatitis B virus genomes isolated from black
RT African patients with fulminant hepatitis B.";
RL J. Med. Virol. 65:485-492 (2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=80;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RX MEDLINE=21361467; PubMed=11468728;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults
RT positive for hepatitis B surface antibody alone: possible association
RT with recombination between genotypes A and D.";
RL J. Med. Virol. 64:441-454 (2001).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA Owiredu W.K.B.A., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA Owiredu W.K.B.A., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV-Mal14;
RA Sugauchi F., Orito E., Kato H., Suzuki S., Hasegawa I., Sakurai M.,
RA Yoshihara N., Ueda R., Mizokami M.;
RT "Hepatitis B virus isolates in Malawi: genotypes, HBsAg subtypes and
RT phylogenetic characterization.";

```

```
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RA Vaishali C., Acharya S.K., Panda S.K.;
RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
sequence of HBV from nine patients with seronegative viral
hepatitis."
RT
RT
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; L13994; AAC31755.1; -
DR EMBL; Z72478; CAA96555.1; -
DR EMBL; X07911; CAA30747.1; -
DR EMBL; AF090841; AAD40214.1; -
DR EMBL; AF090839; AAD40206.1; -
DR EMBL; AF297824; AAK97198.1; -
DR EMBL; AF297819; AAK97177.1; -
DR EMBL; AY128092; AAM96930.1; -
DR EMBL; AB076678; BAC10530.1; -
DR EMBL; AY161138; AAO12546.1; -
DR EMBL; AY161139; AAO12553.1; -
DR PIR; C94409; NKVLA3.
DR PIR; S01405; S01405.
DR PIR; S33686; S33686.
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Nucleocapsid.
SQ SEQUENCE 214 AA; 24643 MW; B7068333FC905D02 CRC64;

Query Match 100.0%; Score 982; DB 12; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.1e-93;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60
DB 30 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 89

QY 61 CWGELMTLATWVGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRTVLEYLV 120
DB 90 CWGELMTLATWVGNLDPASRDLVVYVNTNMGLKIRQLLWFWHISCLTFGRTVLEYLV 149

QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 209

QY 181 RESQC 185
DB 210 RESQC 214

RESULT 6
Q91T09 PRELIMINARY; PRT; 214 AA.
AC Q91T09;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Precore/core protein.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=57;
RX MEDLINE=21361467; PubMed=11468728;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults
positive for hepatitis B surface antibody alone: possible association
with recombination between genotypes A and D."
RL J. Med. Virol. 64:441-454(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=57;
RX MEDLINE=21361467; PubMed=11468728;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults
positive for hepatitis B surface antibody alone: possible association
with recombination between genotypes A and D."
RL J. Med. Virol. 64:441-454(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=79;
RX MEDLINE=21479634; PubMed=11596083;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Molecular analysis of hepatitis B virus genomes isolated from black
African patients with fulminant hepatitis B."
RL J. Med. Virol. 65:485-492(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=79;
RX MEDLINE=21479634; PubMed=11596083;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=57;
RX MEDLINE=21361467; PubMed=11468728;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults
positive for hepatitis B surface antibody alone: possible association
with recombination between genotypes A and D."
RL J. Med. Virol. 64:441-454(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=57;
RX MEDLINE=21361467; PubMed=11468728;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF297622; AAK97190.1; -
DR EMBL; AF297620; AAK97181.1; -
DR PIR; C93460; NKVLA6.
DR PIR; C94409; NKVLA3.
DR PIR; S33686; S33686.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 214 AA; 24642 MW; DC6B2B852CD14953 CRC64;

Query Match 99.7%; Score 979; DB 12; Length 214;
Best Local Similarity 99.5%; Pred. No. 6.3e-93;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
Qy 61 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
Qy 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 209
Qy 181 RESQC 185
Db 210 RESQC 214

RESULT 11
Q91E11 PRELIMINARY; PRT; 185 AA.
AC Q91E11;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Core protein.
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN RA
RP KAY A.C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Jeantet D., Chemin I., Mandrand B., Zoulim P., Trepo C., Hay A.;
RT "Genotype A HBV genomes from a chronic hepatitis B patient.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309370; CAC51285.1; -.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
SQ SEQUENCE 185 AA; 21435 MW; 83162C6382434293 CRC64;

Query Match 99.4%; Score 976; DB 12; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.1e-92;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Qy 61 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 61 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Qy 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 12
Q8JXG8 PRELIMINARY; PRT; 185 AA.
AC Q8JXG8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein.
GN C.
OS Hepatitis B virus.
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OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN RA
RP KAY A.C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB064314; BAB2406.1; -.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
SQ SEQUENCE 185 AA; 21455 MW; D3073D6385AA21A8 CRC64;

Query Match 99.4%; Score 976; DB 12; Length 185;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Qy 61 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 61 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Qy 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 13
Q91E12 PRELIMINARY; PRT; 214 AA.
AC Q91E12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Precore protein.
GN PREC.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN RA
RP KAY A.C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Jeantet D., Chemin I., Mandrand B., Zoulim P., Trepo C., Hay A.;
RT "Genotype A HBV genomes from a chronic hepatitis B patient.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309370; CAC51284.1; -.
DR PIR; S33686; NKVLA3.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
SQ SEQUENCE 214 AA; 24683 MW; E7179233BF287B39 CRC64;

Query Match 99.4%; Score 976; DB 12; Length 214;
Best Local Similarity 98.9%; Pred. No. 1.3e-92;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
Qy 61 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
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Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 209
Qy 181 RESQC 185
Db 210 RESQC 214

RESULT 14

Q8VBG6 PRELIMINARY; PRT; 185 AA.
AC Q8VBG6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Core protein.
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U4;
RA Jazayeri M., Sran N., Gish R., Basuni A.A., Cooksley G., Locarnini S.,
RA Carman W.F.;
RT "HBV core sequence: definition of genotype-specific variability and
RT correlation with geographic origin."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF324120; AAL31833.1; -;
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 185 AA; 21366 MW; D6EC79EE61D8D72D CRC64;

Query Match 99.3%; Score 975; DB 12; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.4e-92;
Matches 183; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVQLLSFLPSDFPSPVRDLDTASALYQEALESPEHCSPHHTALRQAIL 60
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Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 15

Q8BCB5 PRELIMINARY; PRT; 185 AA.
ID Q8BCB5;
AC Q8BCB5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Core protein.
GN C.
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Farekh S., Zoulim F., Tong S.;
RT "Extremely high replication capacity of some hepatitis B virus core
RT promoter mutants."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF537371; AAN15120.1; -;

DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 185 AA; 21422 MW; B86840D541BA70F9 CRC64;

Query Match 99.3%; Score 975; DB 12; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.4e-92;
Matches 183; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Qy 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Db 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

Search completed: July 20, 2004, 09:20:16
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2004, 09:15:04 ; Search time 13 Seconds
(without alignments)
740.998 Million cell updates/sec

Title: US-10-068-059-2
Perfect score: 982
Sequence: 1 MDIDPYKFGATVLLSFLP.....RRRSQSPRRRSQSRSEQ 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	99.7	185	1 CORA_HPBVM	P03149 hepatitis b
2	971	98.9	185	1 CORA_HPBV2	P03148 hepatitis b
3	963	98.1	214	1 CORA_HPBV9	P17099 hepatitis b
4	946	96.3	183	1 CORA_HPBVJ	P17391 hepatitis b
5	940	95.7	183	1 CORA_HPBVY	P03145 hepatitis b
6	932	94.9	183	1 CORA_HPBVO	P17392 hepatitis b
7	932	94.9	183	1 CORA_HPBVZ	P03147 hepatitis b
8	931	94.8	183	1 CORA_HPBV4	P03150 hepatitis b
9	928	94.5	195	1 CORA_HPBVF	P29178 hepatitis b
10	926	94.3	183	1 CORA_HPBVL	P12901 hepatitis b
11	926	94.3	211	1 CORA_HPBVA	P24023 hepatitis b
12	923	94.0	212	1 CORA_HPBVT	Q05495 hepatitis b
13	687.5	70.0	188	1 CORA_HBV1	P03152 woodchuck h
14	681	69.3	217	1 CORA_HPBGS	P03153 ground squi
15	672	68.4	187	1 CORA_HBV8	P06433 woodchuck h
16	174	17.7	305	1 CORA_HPBHE	P13845 heron hepat
17	165.5	16.9	305	1 CORA_HPBDC	P10027 duck hepati
18	163.5	16.6	305	1 CORA_HPBDB	P17190 duck hepati
19	160.5	16.3	305	1 CORA_HPBWB	P17191 duck hepati
20	159.5	16.2	305	1 CORA_HPBDU	P03154 duck hepati
21	97	9.9	196	1 SFR2_CAEEL	Q09511 caenorhabdi
22	96.5	9.8	1007	1 PR4B_HUMAN	Q13523 homo sapien
23	96.5	9.8	1007	1 PR4B_MOUSE	Q61136 mus musculu
24	95.5	9.7	484	1 SFRB_HUMAN	Q05519 homo sapien
25	92	9.4	951	1 SFRB_HUMAN	Q12872 homo sapien
26	91	9.3	253	1 GX42_RAT	Q10021 rattus norv
27	90.5	9.2	208	1 YSX2_CAEEL	Q10021 caenorhabdi
28	90.5	9.2	955	1 T150_HUMAN	Q9Y2W1 homo sapien
29	89	9.1	1654	1 PCFB_HUMAN	Q94913 homo sapien
30	86	8.8	61	1 HSP1_MACEU	P42138 macropus eu
31	86	8.8	306	1 RM45_MOUSE	Q9D0Q7 mus musculu
32	85	8.7	253	1 GX42_MOUSE	Q91XR9 mus musculu
33	83.5	8.5	219	1 NOL3_HUMAN	O60936 homo sapien

ALIGNMENTS

RESULT 1

CORA_HPBVM

ID CORA_HPBVM STANDARD; PRT; 185 AA.

AC P03149; 1986 (Rel. 01, Created)

DT 21-JUN-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-1989 (Rel. 12, Last annotation update)

DE Core antigen.

GN C.

OS Hepatitis B virus (subtype adw).

OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=106821;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83168919; PubMed=6300776;

RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;

RT "The complete nucleotide sequences of the cloned hepatitis B virus

DNA; subtype adr and adw.";

RL Nucleic Acids Res. 11:1747-1757(1983).

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DR EMBL; V00866; -; NOT_ANNOTATED_CDS.

DR InterPro; IPR002006; Hepatitis_core.

DR Pfam; PF00906; Hepatitis_core; 1.

KW Core protein; Repeat.

FT REPEAT 164 171

FT REPEAT 172 179

SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;

Query Match

Best Local Similarity 99.7%; Score 979; DB 1; Length 185;

Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy

1 MDIDPYKFGATVLLSFLPSDFPSPVRLDLDTSALYREALSPHCSPHHTALROAIL 60

Db

1 MDIDPYKFGATVLLSFLPSDFPSPVRLDLDTSALYREALSPHCSPHHTALROAIL 60

Qy

61 CWGELMTLATVWGNLDDPASRDILVNVYVNTNMGKIRQLLWFIHISCLTFGRETVEYL 120

Db

61 CWGELMTLATVWGNLDDPASRDILVNVYVNTNMGKIRQLLWFIHISCLTFGRETVEYL 120

Qy

121 SFGWINTPPAYPPNAPILSTLPETTVRRRRDRGRSPRRTPSPRRRSQS 180

Db

121 SFGWINTPPAYPPNAPILSTLPETTVRRRRDRGRSPRRTPSPRRRSQS 180

Qy

181 RESQC 185

Db

181 RESQC 185

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RESULT 2
CORAS_HPBV2
ID CORA_HPBV2 STANDARD; PRT; 185 AA.
AC P03148;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1990 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
  (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
  RL Animal virus genetics, pp.57-70. Academic Press, New York (1980).
DR InterPro; IPR002006; Hepatitis_core.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 98.9%; Score 971; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 4.8e-83;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGNLDPASRDVLVYVNTNMGKIRQLLWFIHISCLTFGRETVEYLIV 120
DB 61 CWGELMTLATWGNLDPASRDVLVYVNTNMGKIRQLLWFIHISCLTFGRETVEYLIV 120
QY 121 SFGWIRTTPAYPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB 121 SFGWIRTTPAYPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 3
CORAS_HPBV9
ID CORA_HPBV9 STANDARD; PRT; 214 AA.
AC P17059;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koehel H.G., Schueler A., Lottmann S., Thomassen R.;
  Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
RL -----
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CC -----
DR EMBL; X51970; CAA36232.1; -
DR PIR; S10381; NKVLKS.

RESULT 4
CORAS_HPBVJ
ID CORA_HPBVJ STANDARD; PRT; 183 AA.
AC P17391;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Japan/pJDM233).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tenda F., Sakugawa H., Sastrosowiguno R.I., Imai M.,
  Miyakawa Y., Mayumi M.;
  RT "Typing hepatitis B virus by homology in nucleotide sequence:
  comparison of surface antigen subtypes.";
  J. Gen. Virol. 69:2575-2583(1988).
RL -----
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CC -----
DR EMBL; D00329; -; NOT_ANNOTATED_CDS.
DR PIR; A28925; NKVLJ1.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5FAF5E160 CRC64;

Query Match 96.3%; Score 946; DB 1; Length 183;
Best Local Similarity 97.3%; Pred. No. 9.9e-81;
Matches 180; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
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DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 98.1%; Score 963; DB 1; Length 214;
Best Local Similarity 98.9%; Pred. No. 3.1e-82;
Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 30 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGNLDPASRDVLVYVNTNMGKIRQLLWFIHISCLTFGRETVEYLIV 120
DB 90 CWGELMTLATWGNLDPASRDVLVYVNTNMGKIRQLLWFIHISCLTFGRETVEYLIV 149
QY 121 SFGWIRTTPAYPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB 150 SFGWIRTTPAYPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 209
QY 181 RESQC 185
DB 210 RESQC 214
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Qy 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Db 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRR--RGRSPRRRTSPRRRSQSPRRRSQS 178
Qy 181 RESQC 185
Db 179 RESQC 183

RESULT 5
CORR_HPBV
ID CORR_HPBV STANDARD; PRT; 183 AA.
AC P03146;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
   cloned in E. coli.";
RL Nature 281:646-650(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Latvia;
RC MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Pushko P., Dreilina D., Pumpen P., Gren E.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
   analysis.";
RL FEBS Lett. 185:208-212(1985).

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-----
EMBL; V01460; CAA24706.1; ALT INIT.
EMBL; X02496; -; NOT ANNOTATED CDS.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
FT VARIANT 33 33 T -> N (IN STRAIN LATVIA).
FT VARIANT 80 80 A -> I (IN STRAIN LATVIA).
SQ SEQUENCE 183 AA; 21116 MW; E0D9D9763F24E958 CRC64;

Query Match 95.7%; Score 940; DB 1; Length 183;
Best Local Similarity 96.8%; Pred No. 3.6e-80;
Matches 179; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 1 MDIDPKFPGATVELLSFLPSDFPVRDLDTASALYREALSEPHCSPHHTALQAIL 60
Db 1 MDIDPKFPGATVELLSFLPSDFPVRDLDTASALYREALSEPHCSPHHTALQAIL 60
Qy 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Db 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRR--RGRSPRRRTSPRRRSQSPRRRSQS 178
Qy 181 RESQC 185
Db 179 RESQC 183

RESULT 6
CORR_HPBV
ID CORR_HPBV STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Inai M.,
   Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
   comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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-----
EMBL; D00330; -; NOT ANNOTATED CDS.
PIR; B28925; NKVLJ2.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 66BDB2633122930C CRC64;

Query Match 94.9%; Score 932; DB 1; Length 183;
Best Local Similarity 95.7%; Pred. No. 2e-79;
Matches 177; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 MDIDPKFPGATVELLSFLPSDFPVRDLDTASALYREALSEPHCSPHHTALQAIL 60
Db 1 MDIDPKFPGATVELLSFLPSDFPVRDLDTASALYREALSEPHCSPHHTALQAIL 60
Qy 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Db 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRR--RGRSPRRRTSPRRRSQSPRRRSQS 178
Qy 181 RESQC 185
Db 179 RESQC 183

RESULT 7
CORR_HPBV
ID CORR_HPBV STANDARD; PRT; 183 AA.
AC P03147;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)

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Db 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRR--RGRSPRRRTSPRRRSQSPRRRSQS 178
Qy 181 RESQC 185
Db 179 RESQC 183

RESULT 6
CORR_HPBV
ID CORR_HPBV STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Inai M.,
   Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
   comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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-----
EMBL; D00330; -; NOT ANNOTATED CDS.
PIR; B28925; NKVLJ2.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 66BDB2633122930C CRC64;

Query Match 94.9%; Score 932; DB 1; Length 183;
Best Local Similarity 95.7%; Pred. No. 2e-79;
Matches 177; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 MDIDPKFPGATVELLSFLPSDFPVRDLDTASALYREALSEPHCSPHHTALQAIL 60
Db 1 MDIDPKFPGATVELLSFLPSDFPVRDLDTASALYREALSEPHCSPHHTALQAIL 60
Qy 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Db 61 CWGELMTLATWVGNNLEDPASDLVYVNTNMGLKIRQLLWFWHISCLTGTRETLYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db 121 SFGVWIRTPPAYRPPNAPILSTLTPTTAVRR--RGRSPRRRTSPRRRSQSPRRRSQS 178
Qy 181 RESQC 185
Db 179 RESQC 183

RESULT 7
CORR_HPBV
ID CORR_HPBV STANDARD; PRT; 183 AA.
AC P03147;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)

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RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RL a persistently infected homosexual man.";
RL Hepatology 11:271-276(1990).
DR PIR, A37182; NKVLH3.
DR InterPro: IPR002006; Hepatitis core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
FT REPEAT 182 189
SQ SEQUENCE 195 AA; 22461 MW; E2B166F879CB7CB7 CRC64;

Query Match 94.5%; Score 928; DB 1; Length 195;
Best Local Similarity 95.7%; Pred. No. 5e-79;
Matches 177; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 13 LDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYRESLESDDHCSPHHTALRQAIL 72

Qy 61 CWGELMTLATVWGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYL 120
Db 73 CWELMTLATVWGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYL 132

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGSRPRRTTPSPRRRSOSPRRRRSQS 180
Db 133 SFGWIRTPPAYRPPNAPILSTLPTTVVRR--RGRSPRRTPSPRRRSOSPRRRRSQS 190

Qy 181 RESQC 185
Db 191 RESQC 195

RESULT 10
CORR HPBVL STANDARD; PRT; 183 AA.
AC P12501.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain lah / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP MEDLINE=88258473; PubMed=2038576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).
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CC -----
DR EMBL; D00220; BAA00157.1; -
DR PIR; A28885; NKVLCP.
DR PDB; 1HHH; 31-OCT-93.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat; 3D-structure.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 20999 MW; 923DCB94A33FC0E8 CRC64;
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Query Match 94.3%; Score 926; DB 1; Length 183;
Best Local Similarity 95.7%; Pred. No. 7.1e-79;
Matches 177; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60

Qy 61 CWGELMTLATVWGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYL 120
Db 61 CWGELMTLATVWGNLNLEDPASREQVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYL 120

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGSRPRRTTPSPRRRSOSPRRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRR--RGRSPRRTPSPRRRSOSPRRRRSQS 178

Qy 181 RESQC 185
Db 179 PASQC 183

RESULT 11
CORR HPBVA STANDARD; PRT; 211 AA.
ID CORR HPBVA STANDARD; PRT; 211 AA.
AC P24023.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
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CC -----
DR EMBL; M32138; -; NOT_ANNOTATED_CDS.
DR PIR; A34773; NKVLAL.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 183 190
FT REPEAT 198 206
SQ SEQUENCE 211 AA; 24208 MW; B774AC72E65C75AB CRC64;

Query Match 94.3%; Score 926; DB 1; Length 211;
Best Local Similarity 94.1%; Pred. No. 8.3e-79;
Matches 174; Conservative 6; Mismatches 3; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 29 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 88

Qy 61 CWGELMTLATVWGNLNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYL 120
Db 89 CWGLITLITWVGNGNLEDPDTSRDLVVSVYVNTNMGLKIRQLLWFHISCLTFGRETVEYL 148

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGSRPRRTTPSPRRRSOSPRRRRSQS 180
Db 149 SFGWIRTPPAYRPPNAPILSTLPTTVVRR--RGRSPRRTPSPRRRSOSPRRRRSQS 206
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Qy 181 RESQC 185
Db 207 RESQC 211

RESULT 12
CORA HBVT
ID CORA HBVT STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Core antigen.
DE C.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4."
RL J. Gen. Virol. 74:1627-1632(1993).
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CC -----
CC EMBL; X69798; CAA49452.1; -
DR PIR; J02227.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT DOMAIN 178 204 ARG-RICH.
FT DOMAIN 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.
FT REPEAT 184 188 1.
FT REPEAT 191 195 2.
FT REPEAT 199 203 3.
FT SEQUENCE 212 AA; 24234 MW; F832610DB7C36FD2 CRC64;

Query Match 94.0%; Score 923; DB 1; Length 212;
Best Local Similarity 94.6%; Pred. No. 1.6e-78;
Matches 175; Conservative 6; Mismatches 2; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGASVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
Qy 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWPHISCLTGTGRTVLEYLV 120
Db 90 CWGELMTLASWGNLDPARDLVVYVNTNMGLKIRQLLWPHISCLTGTGRTVLEYLV 149
Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRRTSPRRRSQS 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVRR--RGRSPRRRTSPRRRSQS 207
Qy 181 RESQC 185
Db 208 PASQC 212

RESULT 13
CORA WHV1
ID CORA WHV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
DE C.
OS Woodchuck hepatitis virus 1 (WHV 1),
OS Woodchuck hepatitis virus 7 (WHV 7),
OS Woodchuck hepatitis virus 59 (WHV 59), and
OS Woodchuck hepatitis virus 8 (infectious clone) (WHV 8).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10430, 10432, 10431, 10434;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=Woodchuck hepatitis virus 1;
RX MEDLINE=82216969; PubMed=7086958;
RA Gallibert F., Chen T.N., Mandart E.;
RA "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence."
RL J. Virol. 41:51-65(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=Woodchuck hepatitis virus 7, and Woodchuck hepatitis virus 59;
RX MEDLINE=88101359; PubMed=3336938;
RA Cohen J.I., Miller R.H., Rosenblum B., Denniston K., Gerin J.L.,
RA Purcell R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome."
RL Virology 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=Woodchuck hepatitis virus 8 (infectious clone);
RX MEDLINE=89184524; PubMed=2928306;
RA Girones R., Cote P.J., Hornbuckle W.E., Tennant B.C., Gerin J.L.,
RA Purcell R.H., Miller R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host."
RL Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
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CC -----
CC EMBL; J02442; AAA46761.1; -
DR EMBL; M18752; AAA46769.1; -
DR EMBL; M19183; AAA46765.1; -
DR EMBL; J04514; AAA46772.1; -
DR PIR; C32397; NKVLC.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 167 174
FT REPEAT 175 182
FT SEQUENCE 188 AA; 21693 MW; 1P4454D0A7B7CE42 CRC64;

Query Match 70.0%; Score 687.5; DB 1; Length 188;
Best Local Similarity 67.0%; Pred. No. 9.5e-57;
Matches 126; Conservative 22; Mismatches 37; Indels 3; Gaps 1;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGSSYQLLNFLDFFDLDNALVDTATLYEEETGHCSPHHTALRQALV 60
Qy 61 CWGELMTLATWGNLDPASRDLVVYVNTNMGLKIRQLLWPHISCLTGTGRTVLEYLV 120
Db 61 CWDELTKLIAMSSNITTSQVRTIIVNVNDTWGLKVRQSLWFLHLSCLTGTGHTVCEFLV 120
Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVRRDR--RGRSPRRRTSPRRRSQS 177
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVRR--RGRSPRRRTSPRRRSQS 180

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QY 178 SQRESOC 185
DB 181 SQSPSANC 188

RESULT 14
CORA HPBGS
ID CORA HPBGS STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE Core antigen.
GN C.
OS Ground squirrel hepatitis virus (GSV).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10406;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84267998; PubMed=6086950;
RA Seeger C., Ganem D., Varmus H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
RL J. Virol. 51:367-375(1984).
CC
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CC
CC EMBL; K02715; AAA46755.1; -.
DR PIR; A03715; NKVLS.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; DF489467355EC11A CRC64;

Query Match 69.3%; Score 681; DB 1; Length 217;
Best Local Similarity 67.6%; Pred. No. 4.5e-56;
Matches 127; Conservative 21; Mismatches 36; Indels 4; Gaps 2;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDDTASALYREALSPERHCSPHHTALRQAIL 60
DB 31 MDIDPYKEFGSSYQLLNFLPLDFFPDNLALVDTAALYEEELTGREHCSPHHTAIRQALV 90
QY 61 CWGELMTLATWVGNLDPASRDVYVYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
DB 91 CWELTLITWMSNTTEEVRR--IIVDVNNTWGLKVRQLTLWFLSLCLTFGQHTVQEFV 149
QY 121 SFGVWIRTPPYRPPNAPILSTLPTETTVRRD---RGRSPRRTPSPRRRSQSPRRR 177
DB 150 SFGVWIRTPPYRPPNAPILSTLPTETTVIRRGSGRAARSPPRRTPSPRRRSQSPRRR 209
QY 178 SQRESOC 185
DB 210 SQSPASNC 217

RESULT 15
CORA WHV8
ID CORA WHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Woodchuck hepatitis virus 8 (WHV 8).
```

```
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10433;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86062931; PubMed=3855246;
RA Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RL J. Virol. 56:978-986(1985).
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CC
CC EMBL; M11082; AAA19185.1; -.
DR PIR; A03714; NKVLC2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; 21579 MW; D4BC4466FF7163165 CRC64;

Query Match 68.4%; Score 672; DB 1; Length 187;
Best Local Similarity 66.3%; Pred. No. 2.6e-55;
Matches 124; Conservative 22; Mismatches 39; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDDTASALYREALSPERHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGSSYQLLNFLPLDFFPDNLALVDTAALYEEELTGREHCSPHHTAIRQALV 60
QY 61 CWGELMTLATWVGNLDPASRDVYVYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLV 120
DB 61 CWDELTKLIAWSSNITSEQVRTIIIVHVDNTWGLKVRQLTLWFLSLCLTFGQHTVQEFV 120
QY 121 SFGVWIRTPPYRPPNAPILSTLPTETTVRR--RDRGRSPRRTPSPRRRSQSPRRR 178
DB 121 SFGVWIRTPPYRPPNAPILSTLPTETTVIRRGGARASRSPRRTPSPRRRSQSPRRR 180
QY 179 QSRESOC 185
DB 181 QSPSANC 187

Search completed: July 20, 2004, 09:19:24
Job time : 14 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2004, 09:16:24 ; Search time 16 Seconds
(without alignments)
1112.215 Million cell updates/sec

Title: US-10-068-059-2

Perfect score: 982
Sequence: 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRSQSRESQC 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	982	100.0	214	2 S01405	core antigen - hep
2	979	99.7	214	1 NKVLA6	e antigen precursor
3	977	99.5	214	2 S47409	e antigen precursor
4	973	99.1	214	2 S33686	e antigen precursor
5	972	99.0	214	1 NKVLA3	e antigen precursor
6	963	98.1	214	1 NKVLKS	e antigen precursor
7	946	96.3	212	1 NKVLJ1	e antigen precursor
8	946	96.3	212	2 S25651	e antigen precursor
9	940	95.7	212	1 NKVLAH	e antigen precursor
10	938	95.5	212	2 S53227	e antigen precursor
11	937	95.4	212	2 S53211	e antigen precursor
12	937	95.4	212	2 S32204	e antigen precursor
13	937	95.4	212	2 S20750	e antigen precursor
14	935	95.2	183	2 S53169	core antigen - hep
15	935	95.2	212	2 S53216	e antigen precursor
16	935	95.2	212	2 S53253	e antigen precursor
17	935	95.2	212	2 S53272	e antigen precursor
18	934	95.1	212	2 S53225	e antigen precursor
19	934	95.1	212	2 S53274	e antigen precursor
20	934	95.1	212	2 S53163	e antigen precursor
21	933	95.0	212	1 NKVLBH	e antigen precursor
22	932	94.9	183	1 NKVLA2	core antigen - hep
23	932	94.9	212	1 NKVLJ2	e antigen precursor
24	932	94.9	212	2 S53240	e antigen precursor
25	931	94.8	183	2 S53247	core antigen - hep
26	931	94.8	183	2 S53270	e antigen precursor
27	931	94.8	212	1 NKVLA4	e antigen precursor
28	931	94.8	212	2 S53251	e antigen precursor
29	931	94.8	212	2 S20746	e antigen precursor

30	930	94.7	212	2 S53242	e antigen precursor
31	930	94.7	212	2 S53159	e antigen precursor
32	930	94.7	212	2 S53200	e antigen precursor
33	930	94.7	212	2 S53202	e antigen precursor
34	929	94.6	212	2 S53281	e antigen precursor
35	929	94.6	212	2 S53198	e antigen precursor
36	928	94.5	183	2 S53152	core antigen - hep
37	928	94.5	195	1 NKVLH3	core antigen - hep
38	928	94.5	212	2 S53223	e antigen precursor
39	928	94.5	359	2 S04570	gene X/C fusion pr
40	926	94.3	183	1 NKVLCP	core antigen - hep
41	926	94.3	211	1 NKVLA1	e antigen precursor
42	925	94.2	212	2 S53204	e antigen precursor
43	924	94.1	212	2 S53229	e antigen precursor
44	923	94.0	183	2 S53232	core antigen - hep
45	923	94.0	183	2 S53260	core antigen - hep

ALIGNMENTS

RESULT 1

S01405
core antigen - hepatitis B virus
N:Alternate names: nucleocapsid protein
C:Species: hepatitis B virus, HBV
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 26-Aug-1999
C:Accession: S01405
R:Cheng, S.; Vogel, R.; Ye, W.; Blume, M.; Lee, S.; Hung, P.
Nucleic Acids Res. 16, 8188, 1988
A:Title: The core gene of hepatitis B virus; subtype adw2.
A:Reference number: S01405; MUID:88355570; PMID:3419915
A:Accession: S01405
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-214 <CHS>
A:Cross-references: EMBL:X07911; NID:G59446; PIDN:CAA30747.1; PID:G59447
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1988
C:Superfamily: Hepatitis B virus core antigen
C:Keywords: nucleocapsid

Query Match	100.0%;	Score 982;	DB 2;	Length 214;
Best Local Similarity	100.0%;	Pred. No. 1.1e-79;		
Matches	185;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALQAIL	60	
Db	30	MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALQAIL	89	
Qy	61	CWGLMTLATWVGNLDPASRDVLVNYVNTNMGLKIRQLLWPHISCLTGTGRETVLEYLV	120	
Db	90	CWGLMTLATWVGNLDPASRDVLVNYVNTNMGLKIRQLLWPHISCLTGTGRETVLEYLV	149	
Qy	121	SPGWITTPPAYPPNAPILSTLPTTVVRRRDRGRSPRRTPSPRRRSQSPPRRRSQS	180	
Db	150	SPGWITTPPAYPPNAPILSTLPTTVVRRRDRGRSPRRTPSPRRRSQSPPRRRSQS	209	
Qy	181	RESQC 185		
Db	210	RESQC 214		

RESULT 2

NKVLA6
e antigen precursor / core antigen - hepatitis B virus (subtype adw)
N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype adw
C>Date: 30-Jun-1992 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
C:Accession: C93460; A03711
R:Ono, Y.; Onda, H.; Saeada, R.; Igarashi, K.; Sugino, Y.; Nishioaka, K.
Nucleic Acids Res. 11, 1747-1757, 1983

A;Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype
A;Reference number: A93460; MUID:83168919; PMID:6300776
A;Accession: C93460
A;Molecule type: DNA
A;Residues: 1-214 <ONO>
A;Cross-references: GB:V00866
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-214/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-214/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>
Query Match 99.7%; Score 979; DB 1; Length 214;
Best Local Similarity 99.5%; Pred. No. 2e-79;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLSPDPPSVDRDLDTASALYREALSPHCSPHHTALQAIL 60
DB 30 MDIDPYKEFGATVELLSFLSPDPPSVDRDLDTASALYREALSPHCSPHHTALQAIL 89
QY 61 CWGELMTLATWGNLDPASRDLVVNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
DB 90 CWGELMTLATWGNLDPASRDLVVNTNMGKIRQLLWPHISCLTFGRETVEYLIV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 209
QY 181 RESQC 185
DB 210 RESQC 214
RESULT 3
S47409
e antigen precursor / core antigen - hepatitis B virus (subtype adw2)
N;Alternate names: HBe antigen precursor / Hbc antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S47409
R;Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolat
A;Reference number: S47404
A;Accession: S47409
A;Molecule type: DNA
A;Residues: 1-214 <PLU>
A;Cross-references: EMBL:235717; MID:9527440; PIDN:CAA84790.1; PID:9527442
A;Experimental source: subtype adw2
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-214/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-214/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>
Query Match 99.5%; Score 977; DB 2; Length 214;
Best Local Similarity 99.5%; Pred. No. 3e-79;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLSPDPPSVDRDLDTASALYREALSPHCSPHHTALQAIL 60
DB 30 MDIDPYKEFGATVELLSFLSPDPPSVDRDLDTASALYREALSPHCSPHHTALQAIL 89
QY 61 CWGELMTLATWGNLDPASRDLVVNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120

DB 90 CWGELMTLATWGNLDPASRDLVVNTNMGKIRQLLWPHISCLTFGRETVEYLIV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 209
QY 181 RESQC 185
DB 210 RESQC 214
RESULT 4
S33686
e antigen precursor / core antigen - hepatitis B virus (subtype adw2; patient A938)
N;Alternate names: HBe antigen precursor / Hbc antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2, patient A938
C;Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
C;Accession: S33686
R;Preisler-Adams, S.; Schlayer, H.J.; Peters, T.; Korp, R.; Rasenack, J.
Nucleic Acids Res. 21, 2258, 1993
A;Title: Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identif
A;Reference number: S33686; MUID:93275766; PMID:8502574
A;Accession: S33686
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-214 <PRE>
A;Cross-references: EMBL:X70185
A;Experimental source: subtype adw2, patient A938
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-214/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-214/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>
Query Match 99.1%; Score 973; DB 2; Length 214;
Best Local Similarity 99.5%; Pred. No. 6.9e-79;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLSPDPPSVDRDLDTASALYREALSPHCSPHHTALQAIL 60
DB 30 MDIDPYKEFGATVELLSFLSPDPPSVDRDLDTASALYREALSPHCSPHHTALQAIL 89
QY 61 CWGELMTLATWGNLDPASRDLVVNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
DB 90 CWGELMTLATWGNLDPASRDLVVNTNMGKIRQLLWPHISCLTFGRETVEYLIV 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQS 209
QY 181 RESQC 185
DB 210 RESQC 214
RESULT 5
NKVLA3
e antigen precursor / core antigen - hepatitis B virus (subtype adw2)
N;Alternate names: HBe antigen precursor / Hbc antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;Date: 30-Jun-1992 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
C;Accession: C94409; A03711
R;Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Aca
A;Reference number: A94409

A:Accession: C94409
A:Molecule type: DNA
A:Residues: 1-214 <VAL>
A:Cross-references: EMBL:X02763
A:Experimental source: subtype adw2
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-214/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-214/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.0%; Score 972; DB 1; Length 214;
Best Local Similarity 98.9%; Pred. No. 8.4e-79;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 149
Qy 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 209
Qy 181 RESQC 185
Db 210 RESQC 214

RESULT 6
NKVLKS
e antigen precursor / core antigen - hepatitis B virus (subtype adw, strain 991)
N:Alternate names: HBe antigen precursor / HBe antigen, pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype adw isolate HBV 991
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Sep-1997
C:Accession: S10381
R:Koehel, H.G.; Schueler, A.; Lottmann, S.; Thomassen, R.
submitted to the EMBL Data Library, February 1990
A:Reference number: S10380
A:Accession: S10381
A:Molecule type: DNA
A:Residues: 1-214 <KOE>
A:Cross-references: EMBL:X51970; NID:g1155012; PID:g60433
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-214/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-214/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.1%; Score 963; DB 1; Length 214;
Best Local Similarity 98.9%; Pred. No. 5.3e-78;
Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 149
Qy 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180

Db 150 SFGWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 209
Qy 181 RESQC 185
Db 210 RESQC 214

RESULT 7
NKVLJ1
e antigen precursor / core antigen - hepatitis B virus (subtype adw, strain Japan/pJDM2)
N:Alternate names: HBe antigen precursor / HBe antigen, pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype adw, strain Japan/pJDM233
C:Date: 31-Mar-1990 #sequence_revision 08-Nov-1996 #text_change 14-Nov-1997
C:Accession: A28925
R:Okamoto, H.; Tada, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.;
J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur
A:Reference number: J50253; MUID:89010694; PMID:3171552
A:Accession: A28925
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-212 <OKA>
A:Cross-references: EMBL:D00329; NID:g221498
A:Experimental source: subtype adw, strain Japan/pJDM233
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 96.3%; Score 946; DB 1; Length 212;
Best Local Similarity 97.3%; Pred. No. 1.7e-76;
Matches 180; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 149
Qy 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180
Db 150 SFGWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 207
Qy 181 RESQC 185
Db 208 RESQC 212

RESULT 8
S25651
e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient D)
N:Alternate names: HBe antigen precursor / HBe antigen, pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient D
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S25651
R:Lai, M.E.; Mazzoleni, A.P.; Mellis, A.; Balestrieri, A.
submitted to the EMBL Data Library, September 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negat
A:Reference number: S25650
A:Accession: S25651
A:Molecule type: DNA
A:Residues: 1-212 <LAI>

A;Cross-references: EMBL:X8292; NID:G59448; PIDN:CAA48353.1; PID:G59450
A;Experimental source: subtype ayw, patient D
C;Genetics:
A;Gene: C

C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein

F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>

F;30-178/Product: e antigen #status predicted <EAG>

F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <BCP>

Query Match 96.38; Score 946; DB 2; Length 212;

Best Local Similarity 97.38; Pred. No. 1.7e-76;

Matches 180; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHTALRQAIL 60

Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHTALRQAIL 89

Qy 61 CWGELMTLATWGNLDPASDLVYVNTNMGKIRQLLWFIHISCLTFGRVLEYLV 120

Db 90 CWGELMTLATWGNLDPASDLVYVNTNMGKIRQLLWFIHISCLTFGRVLEYLV 149

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRRSQSPRRRSOS 180

Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVRRDR--RSPRRTSPPRRRSQSPRRRSOS 207

Qy 181 RESQC 185

Db 208 RESQC 212

RESULT 9

NKVLAAH

N;Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

N;Contains: core antigen; e antigen

C;Species: hepatitis B virus, HBV

A;Variety: subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient Ca

cheri'83

C;Date: 18-Dec-1981 #sequence revision 08-Nov-1996 #text change 16-Jul-1999

C;Accession: S47405; S53191; S53209; S53234; S53264; S53269; S53277; A03711

R;Plucieniczak, A.

submitted to the EMBL Data Library, August 1994

A;Description: Molecular cloning and sequencing of two complete genomes of polish isolat

A;Reference number: S47404

A;Accession: S47405

A;Molecule type: DNA

A;Residues: 1-212 <PIJ>

A;Cross-references: EMBL:Z35716; NID:G527435; PIDN:CAA84786.1; PID:G527437

A;Experimental source: subtype ayw4, isolate hb321

R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53191

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85283; NID:G736088; PIDN:CAA59593.1; PID:G736090

A;Experimental source: isolate patient Ferracuti'83

A;Accession: S53209

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85290; NID:G736114; PIDN:CAA59609.1; PID:G736116

A;Experimental source: isolate patient Castag'83

A;Accession: S53234

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85300; NID:G736150; PIDN:CAA59631.1; PID:G736152

A;Experimental source: isolate patient Sanna'84

A;Accession: S53264

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85313; NID:G736194; PIDN:CAA59659.1; PID:G736196

A;Experimental source: isolate patient Licheri'1'85

A;Accession: S53249

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85306; NID:G736172; PIDN:CAA59644.1; PID:G736174

A;Experimental source: isolate patient Flore'1'86

A;Accession: S53262

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85312; NID:G736191; PIDN:CAA59657.1; PID:G736193

A;Experimental source: isolate patient Licheri'83

A;Accession: S53277

A;Molecule type: DNA

A;Residues: 30-212 <LAI>

A;Cross-references: EMBL:X85317; NID:G736211; PIDN:CAA59669.1; PID:G736214

A;Experimental source: patient Giorio-2'86

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

R;Calbert, P.; Mandat, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.

Nature 281, 646-650, 1979

A;Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A;Reference number: A93214; MUID:81012091; PMID:399327

A;Accession: A03711

A;Molecule type: DNA

A;Residues: 1-212 <GAL>

A;Cross-references: GB:J02203; NID:G329640; PIDN:AAA45489.1; PID:G329642

A;Experimental source: subtype ayw

C;Genetics:

A;Gene: C

C;Superfamily: hepatitis B virus core antigen

C;Keywords: alternative initiators; core protein

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-212/Product: core antigen #status predicted <CAG>

F;30-178/Product: e antigen #status predicted <EAG>

F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <BCP>

Query Match 95.7%; Score 940; DB 1; Length 212;

Best Local Similarity 96.8%; Pred. No. 5.7e-76;

Matches 179; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHTALRQAIL 60

Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHTALRQAIL 89

Qy 61 CWGELMTLATWGNLDPASDLVYVNTNMGKIRQLLWFIHISCLTFGRVLEYLV 120

Db 90 CWGELMTLATWGNLDPASDLVYVNTNMGKIRQLLWFIHISCLTFGRVLEYLV 149

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRRSQSPRRRSOS 180

Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVRR--RGRSPRRTSPPRRRSQSPRRRSOS 207

Qy 181 RESQC 185

Db 208 RESQC 212

RESULT 10

S53227

e antigen precursor / core antigen - hepatitis B virus (isolate patient Dettori'85 and

N;Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

N;Contains: core antigen; e antigen

C;Species: hepatitis B virus, HBV

A;Variety: isolate patient Dettori'85; isolate patient Chighine'82

C;Date: 28-Oct-1995 #sequence revision 03-Nov-1995 #text change 26-Aug-1999

C;Accession: S53227; S53218

R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53227

A;Molecule type: DNA

A;Residues: 1-212 <LAI>

A;Cross-references: EMBL:X85297; NID:G736140; PIDN:CAA59624.1; PID:G736142

A;Experimental source: isolate patient Dettori'85

A:Accession: S53218
A:Molecule type: DNA
A:Residues: 1-212 <LAW>
A:Cross-references: EMBL:X85294; NID:g736131; PIDN:CAA59618.1; PID:g736133
A:Experimental source: isolate patient Chighine'82
C:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 95.5%; Score 938; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 8.5e-76;
Matches 178; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
Db 208 RESQC 212

Query Match 95.5%; Score 938; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 8.5e-76;
Matches 178; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
Db 208 RESQC 212

Query Match 95.5%; Score 938; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 8.5e-76;
Matches 178; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
Db 208 RESQC 212

Query Match 95.5%; Score 938; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 8.5e-76;
Matches 178; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
Db 208 RESQC 212

Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
Db 208 RESQC 212

RESULT 12
S32204
e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patients C1000 and
N:Alternate names: HBe antigen precursor / Hbc antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Oct-2000
C:Accession: S32204; S53207
R:Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
A:Description: Identification and sequence analysis of hepatitis B virus DNA in immunol.
A:Reference number: S32202
A:Accession: S32204
A:Molecule type: DNA
A:Residues: 1-212 <PR>
A:Cross-references: EMBL:X72702; NID:g288927; PIDN:CAA51257.1; PID:g288930
A:Experimental source: subtype ayw, patient C1000
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53112
A:Accession: S53207
A:Molecule type: DNA
A:Residues: 30-212 <LAI>
A:Cross-references: EMBL:X85289; NID:g736110; PIDN:CAA59607.1; PID:g736113
A:Experimental source: isolate patient Castaa-2'87
A:Note: due to a stop codon mutation between the alternative initiators the e antigen
C:Genetics:
C:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 95.4%; Score 937; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 1e-75;
Matches 178; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
Db 90 CWGELMTLATWVGNLDPASRDVSVYNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 150 SFGVWIRTPPAYRPPNAPILSTLPTTVRRDRGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
Db 208 RESQC 212

RESULT 13
S20750

e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient CI)
N;Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen
C;Species: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw, patient CI
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S20750
R;Jai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A;Reference number: S20745
A;Accession: S20750
A;Molecule type: DNA
A;Residues: 1-212 <LAI>
A;Cross-references: EMBL:X65258; NID:G59434; PIDN:CAA46354.1; PID:G59436
A;Experimental source: subtype ayw, patient CI
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 95.4%; Score 937; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 1e-75;
Matches 178; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 30 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGWIRTPPAYRPPNAPILSTPLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB 150 AFGWIRTPPAYRPPNAPILSTPLPTTVVRR--RGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
DB 208 RESQC 212

RESULT 14
S53169
core antigen - hepatitis B virus (isolate patient Muresu'89)
N;Alternate names: HBC antigen
C;Species: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Muresu'89
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C;Accession: S53169
R;Jai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53169
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: EMBL:X85275; NID:G736057; PIDN:CAA59571.1; PID:G736060
A;Experimental source: isolate patient Muresu'89
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 95.2%; Score 935; DB 2; Length 183;
Best Local Similarity 95.7%; Pred. No. 1.3e-75;
Matches 177; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
DB 61 CWGELMTLATWGVNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
QY 121 SFGWIRTPPAYRPPNAPILSTPLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB 121 SFGWIRTPPAYRPPNAPILSTPLPTTVVRR--RGRTPRRTPSPRRRSQSPRRRSQS 178
QY 181 RESQC 185
DB 179 RESQC 183

RESULT 15

S53216
e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag'3)
N;Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen
C;Species: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Castag'3
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C;Accession: S53216
R;Jai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53216
A;Molecule type: DNA
A;Residues: 1-212 <LAI>
A;Cross-references: EMBL:X85293; NID:G736124; PIDN:CAA59616.1; PID:G736126
A;Experimental source: isolate patient Castag'3
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 95.2%; Score 935; DB 2; Length 212;
Best Local Similarity 96.2%; Pred. No. 1.6e-75;
Matches 178; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 30 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLIV 149
QY 121 SFGWIRTPPAYRPPNAPILSTPLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
DB 150 SFGWIRTPPAYRPPNAPILSTPLPTTVVRR--RGRSPRRTPSPRRRSQSPRRRSQS 207
QY 181 RESQC 185
DB 208 RESQC 212

Search completed: July 20, 2004, 09:20:41
Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2004, 09:18:04 ; Search time 19 Seconds
(without alignments)
502.674 Million cell updates/sec

Title: US-10-068-059-2

Perfect score: 982

Sequence: 1 MDIDPKYKFGATVLLSLFLP.....RRRSQSPRRRSQSRQC 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	982	100.0	185	1	US-07-739-642-2
2	982	100.0	185	1	US-07-739-643-2
3	982	100.0	185	1	US-07-739-142-2
4	982	100.0	185	4	US-08-851-120-6
5	979	99.7	185	3	US-09-248-588-6
6	978	99.6	185	1	US-07-739-642-4
7	978	99.6	185	1	US-07-739-142-4
8	978	99.6	185	1	US-07-739-642-10
9	970	98.8	185	1	US-07-739-643-10
10	970	98.8	185	1	US-07-739-142-10
11	970	98.8	185	1	US-07-739-642-8
12	967	98.5	185	1	US-07-739-643-8
13	967	98.5	185	1	US-07-739-142-8
14	967	98.5	185	3	US-09-248-588-2
15	940	95.7	183	3	US-08-968-747-18
16	940	95.7	194	3	US-08-968-747-3
17	940	95.7	212	3	US-08-968-747-11
18	940	95.7	212	4	US-10-104-966-11
19	940	95.7	346	1	US-08-105-483-217
20	940	95.7	346	1	US-08-709-209-217
21	940	95.7	346	1	US-08-458-101-217
22	935.5	95.3	211	6	5196194-13
23	931	94.8	183	3	US-09-248-588-4
24	927	94.4	183	5	PCT-US96-10602-12
25	925	94.2	183	3	US-08-968-747-20
26	925	94.2	193	3	US-08-968-747-2
27	917	93.4	397	5	PCT-US96-10602-6

28	914.5	93.1	199	3	US-08-968-747-21	Sequence 21, Appl
29	906	92.3	212	4	US-09-719-528A-4	Sequence 4, Appl
30	904	92.1	289	5	PCT-US96-10602-8	Sequence 8, Appl
31	853	86.9	351	5	PCT-US96-10602-4	Sequence 4, Appl
32	811	82.6	214	1	US-07-739-642-6	Sequence 6, Appl
33	811	82.6	214	1	US-07-739-643-6	Sequence 6, Appl
34	811	82.6	214	1	US-07-739-142-6	Sequence 6, Appl
35	802	81.7	214	1	US-07-739-642-12	Sequence 12, Appl
36	802	81.7	214	1	US-07-739-643-12	Sequence 12, Appl
37	802	81.7	214	1	US-07-739-142-12	Sequence 12, Appl
38	775	78.9	159	3	US-08-445-585-3	Sequence 3, Appl
39	752	76.6	154	3	US-08-968-747-1	Sequence 1, Appl
40	752	76.6	155	3	US-08-968-747-17	Sequence 17, Appl
41	752	76.6	161	3	US-08-968-747-19	Sequence 19, Appl
42	687.5	70.0	188	3	US-09-248-588-7	Sequence 7, Appl
43	681	69.3	217	3	US-09-248-588-9	Sequence 9, Appl
44	624	63.5	346	5	PCT-US96-10602-2	Sequence 2, Appl
45	188	19.1	39	3	US-08-968-747-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-07-739-642-2
; Sequence 2, Application US/07739642
; Patent No. 5173427
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Vectors And Hosts With Increased
; TITLE OF INVENTION: Expression Of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739,642
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-642-2

Query Match 100.0%; Score 982; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.4e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDIDPKYKFGATVLLSLFLPSPDFPVRDLDTASALYREALSPHCSPHHTALRAIL 60
Db	1	MDIDPKYKFGATVLLSLFLPSPDFPVRDLDTASALYREALSPHCSPHHTALRAIL 60
Qy	61	CWGLMTLATVGNLLEDPASRLDVVYVNTNMGKIRQLLWPHISCLTFTGRTVLYLV 120
Db	61	CWGLMTLATVGNLLEDPASRLDVVYVNTNMGKIRQLLWPHISCLTFTGRTVLYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db |||||
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db |||||
QY 181 RESQC 185
Db |||||
QY 181 RESQC 185

RESULT 2
US-07-739-643-2
; Sequence 2, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Increased Expression of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739,643
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-643-2

Query Match 100.0%; Score 982; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.4e-101; Mismatches 0; Indels 0; Gaps 0;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db |||||
QY 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Db |||||
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db |||||
QY 181 RESQC 185
Db |||||
QY 181 RESQC 185

RESULT 3
US-07-739-142-2
; Sequence 2, Application US/07739142
; Patent No. 5175272

; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: DNA Sequences With Increased Expression
; TITLE OF INVENTION: of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739,142
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-142-2

Query Match 100.0%; Score 982; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.4e-101; Mismatches 0; Indels 0; Gaps 0;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db |||||
QY 61 CWGELMTLATWGNLDPASRDLVVNYVNTNMGKIRQLLWFHISCLTFGRETVEYLIV 120
Db |||||
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRRTSPRRRSQSPRRRSQS 180
Db |||||
QY 181 RESQC 185
Db |||||
QY 181 RESQC 185

RESULT 4
US-09-851-120-6
; Sequence 6, Application US/09851120
; Patent No. 6479282
; GENERAL INFORMATION:
; APPLICANT: LETOURNEUR, Odile
; APPLICANT: WATELET, Benedicte
; TITLE OF INVENTION: HBC EXPRESSION AND DIAGNOSTIC AND THERAPEUTIC USES
; FILE REFERENCE: 109455
; CURRENT APPLICATION NUMBER: US/09/851,120
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PRT
; ORGANISM: HBV

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US-09-851-120-6
Query Match      100.0%; Score 982; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.4e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Qy 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWFWHISCLTFGRETVEYLIV 120
Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWFWHISCLTFGRETVEYLIV 120

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 5
US-09-248-588-6
; Sequence 6, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; EARLIER FILING DATE: 1999-02-11
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-6

Query Match      99.7%; Score 979; DB 3; Length 185;
Best Local Similarity 99.5%; Pred. No. 5.3e-101;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Qy 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWFWHISCLTFGRETVEYLIV 120
Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWFWHISCLTFGRETVEYLIV 120

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 6
US-07-739-642-4
; Sequence 4, Application US/07739642
; Patent No. 5173427
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Vectors And Hosts With Increased
; FILE REFERENCE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

US-09-851-120-6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07739,642
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-642-4

Query Match      99.6%; Score 978; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 6.8e-101;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Qy 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWFWHISCLTFGRETVEYLIV 120
Db 61 CWGELMTLATWVGNLDPASRDLVVNYVNTNMGLKIRQLLWFWHISCLTFGRETVEYLIV 120

Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 7
US-07-739-643-4
; Sequence 4, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Increased Expression of HBcAg
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/07/739,643
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-739-643-4

Query Match 99.6%; Score 978; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 6.8e-101;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALROAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALROAIL 60
QY 61 CWGELMTLATWGNLNLEDPASRDVLVYVNTNMGKIRQLLWPHFISCLTFGRETVEYL 120
DB 61 CWGELMTLATWGNLNLEDPASRDVLVYVNTNMGKIRQLLWPHFISCLTFGRETVEYL 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 8
US-07-739-142-4
Sequence 4, Application US/07739142
Patent No. 5175272
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: DNA Sequences With Increased Expression
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
US-07-739-142-4
Query Match 99.6%; Score 978; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 6.8e-101;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALROAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALROAIL 60
QY 61 CWGELMTLATWGNLNLEDPASRDVLVYVNTNMGKIRQLLWPHFISCLTFGRETVEYL 120
DB 61 CWGELMTLATWGNLNLEDPASRDVLVYVNTNMGKIRQLLWPHFISCLTFGRETVEYL 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRTPSPRRRSQS 180
QY 181 RESQC 185
DB 181 RESQC 185

RESULT 9
US-07-739-642-10
Sequence 10, Application US/07739642
Patent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Vectors And Hosts With Increased
TITLE OF INVENTION: Expression Of HBCag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,642
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-739-642-10

Query Match 98.8%; Score 970; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.3e-100;
Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALROAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALROAIL 60
QY 61 CWGELMTLATWGNLNLEDPASRDVLVYVNTNMGKIRQLLWPHFISCLTFGRETVEYL 120

Db 61 CWGELMTLATVWGNLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLA 120
Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 10

US-07-739-643-10
; Sequence 10, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Increased Expression of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,643
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-643-10

Query Match 98.8%; Score 970; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.3e-100;
Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAAIL 60
Db 1 MAIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAAIL 60
Qy 61 CWGELMTLATVWGNLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLV 120
Db 61 CWGELMTLATVWGNLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLA 120
Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185

RESULT 11

US-07-739-142-10

; Sequence 10, Application US/07739142
; Patent No. 5175272
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: DNA Sequences With Increased Expression
; TITLE OF INVENTION: of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,142
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-739-142-10

Query Match 98.8%; Score 970; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.3e-100;
Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAAIL 60
Db 1 MAIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAAIL 60
Qy 61 CWGELMTLATVWGNLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLV 120
Db 61 CWGELMTLATVWGNLEDPASRDVNVYVNTNMGLKIRQLLWFHISCLTFGRETVEYLA 120
Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
Qy 181 RESQC 185
Db 181 RESQC 185
RESULT 12
US-07-739-642-8
; Sequence 8, Application US/07739642
; Patent No. 5173427
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Vectors And Hosts With Increased
; TITLE OF INVENTION: Expression of HBCag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.

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; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,642
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
; US-07-739-642-8
;
; Query Match          98.5%; Score 967; DB 1; Length 185;
; Best Local Similarity 98.9%; Pred. No. 1.1e-99;
; Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
; Db 1 MAIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
;
; QY 61 CWGELMTLATWVGNLDPASRDLVVYNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
; Db 61 CWGELMTLATWVGNLDPASRDLVVYNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
;
; QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
; Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
;
; QY 181 RESQC 185
; Db 181 RESQC 185
;
; RESULT 13
; US-07-739-643-8
; Sequence 8, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee,, Richard L.
; TITLE OF INVENTION: Increased Expression of HBCaG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,643
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2090
;
; QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
; Db 1 MAIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
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; QY 61 CWGELMTLATWVGNLDPASRDLVVYNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
; Db 61 CWGELMTLATWVGNLDPASRDLVVYNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
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; QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
; Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
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; QY 181 RESQC 185
; Db 181 RESQC 185
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; RESULT 14
; US-07-739-142-8
; Sequence 8, Application US/07739142
; Patent No. 5175272
; GENERAL INFORMATION:
; APPLICANT: Mallonee,, Richard L.
; TITLE OF INVENTION: DNA Sequences With Increased Expression
; TITLE OF INVENTION: Of HBCaG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,142
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
; US-07-739-142-8
;
; Query Match          98.5%; Score 967; DB 1; Length 185;
; Best Local Similarity 98.9%; Pred. No. 1.1e-99;
; Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
; US-07-739-643-8
;
; Query Match          98.5%; Score 967; DB 1; Length 185;
; Best Local Similarity 98.9%; Pred. No. 1.1e-99;
; Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; Db 1 MAIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
;
; QY 61 CWGELMTLATWVGNLDPASRDLVVYNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
; Db 61 CWGELMTLATWVGNLDPASRDLVVYNTNMGKIRQLLWPHISCLTFGRETVEYLIV 120
;
; QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
; Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180
;
; QY 181 RESQC 185
; Db 181 RESQC 185
;
; RESULT 14
; US-07-739-142-8
; Sequence 8, Application US/07739142
; Patent No. 5175272
; GENERAL INFORMATION:
; APPLICANT: Mallonee,, Richard L.
; TITLE OF INVENTION: DNA Sequences With Increased Expression
; TITLE OF INVENTION: Of HBCaG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,142
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
; US-07-739-142-8
;
; Query Match          98.5%; Score 967; DB 1; Length 185;
; Best Local Similarity 98.9%; Pred. No. 1.1e-99;
; Matches 183; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db	1	MAIDPYKEFGATVELLSFLPSDFPFSVRDLDDTASALYREALSPBHCSPHHTALRQAIL	60
Qy	61	CNGEELMTLATWGNLNEDPASRDLVVNYVNTNMGLKIQLLWFHISCLTFGRETVLEYLV	120
Db	61	CNGEELMTLATWGNLNEDPASRDLVVNYVNTNMGLKIQLLWFHISCLTFGRETVLEYLV	120
Qy	121	SGFWIRTPPAYRPNAPILSTPLPETTVVRREDGRSPRRRTPSRRRSQSPPRRRSOS	180
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Db	181	RESQC 185	

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US-09-248-588-2
; Sequence 2, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-2

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Query Match	95.7%; Score 940; DB 3; Length 183;
Best Local Similarity	96.8%; Pred. No. 1.le-96;
Matches 179; Conservative 2; Mismatches 2; Indels 2; Gaps 1;	
Qy	1 MDIDPYKEFGATVLLSFLPSDDPPSVRDLLDTASALYREALSPHCSPHHTLRQAIL 60.
Dd	1 MDIDPYKEFGATVLLSFLPSDDPPSVRDLLDTASALYREALSPHCSPHHTLRQAIL 60
Qy	61 CWGELMTLATWGVNGLSDPASRDLVVNYVTNNMGLKIQLLWFHISCLITFGETVLYLV 120
Dd	61 CWGELMTLATWGVNGLSDPASRDLVVSYVTNNMGLKFRQLLWFHISCLITFGETVLYLV 120
Qy	121 SFGVWIITPPAYRPNPAPILSTLPETTVRRDRGRSPRRTPSPRRRSQS 180
Dd	121 SFGVWIITPPAYRPNPAPILSTLPETTVVR--RCGRPRRTSPRRRSQS 178
Qy	181 RESQC 185
Dd	179 RESQC 183

Search completed: July 20, 2004, 09:21:11
Job time : 20 secs